

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Keeling, Peter
Guan, Hanping
- (ii) TITLE OF INVENTION: Starch Encapsulation
- (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 - (B) STREET: 5370 Manhattan Circle
 - (C) CITY: Boulder
 - (D) STATE: CO
 - (E) COUNTRY: US
 - (F) ZIP: 80303
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 30-SEP-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/026,855
 - (B) FILING DATE: 30-SEP-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Winner, Ellen P
 - (B) REGISTRATION NUMBER: 28,547
 - (C) REFERENCE/DOCKET NUMBER: 89-97
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (303) 499-8080
 - (B) TELEFAX: (303) 499-8089

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACTAGTCAT ATGGTGAGCA AGGGCGAGGA G

31

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGATCTTC ATATGCTTGT ACAGCTCGTC CATGCC

36

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGATCTTG GCCATGGCCT TGTACAGCTC GTCCATGCC

39

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: join(1449..1553, 1685..1765, 1860..1958, 2055
..2144, 2226..2289, 2413..2513, 2651..2760, 2858
..3101, 3212..3394, 3490..3681, 3793..3879, 3977
..4105, 4227..4343)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCGACCTA TTACACAGCC CGCTCGGGCC CGCGACGTCG GGACACATCT TCTTCCCCCT	60
TTTGGTGAAG CTCTGCTCGC AGCTGTCCGG CTCCTTGGAC GTTCGTGTGG CAGATTCATC	120
TGTTGTCTCG TCTCCTGTGC TTCCTGGGTA GCTTGTGTAG TGGAGCTGAC ATGGTCTGAG	180
CAGGCTTAAA ATTTGCTCGT AGACGAGGAG TACCAGCACA GCACGTTGCG GATTTCTCTG	240

CCTGTGAAGT GCAACGTCTA GGATTGTCAC ACGCCTTGGT CGCGTCGCGT CGCGTCGCGT	300
CGATGCGGTG GTGAGCAGAG CAGCAACAGC TGGGCGGCCC AACGTTGGCT TCCGTGTCTT	360
CGTCGTACGT ACGCGCGCGC CGGGGACACG CAGCAGAGAG CGGAGAGCGA GCCGTGCACG	420
GGGAGGTGGT GTGGAAGTGG AGCCGCGCGC CCGGCCGCCC GCGCCCGGTG GGCAACCCAA	480
AAGTACCCAC GACAAGCGAA GGCGCCAAAG CGATCCAAGC TCCGGAACGC AACAGCATGC	540
GTCGCGTCGG AGAGCCAGCC ACAAGCAGCC GAGAACCGAA CCGGTGGGCG ACGCGTCATG	600
GGACGGACGC GGGCGACGCT TCCAAACGGG CCACGTACGC CGGCGTGTGC GTGCGTGCAG	660
ACGACAAGCC AAGGCGAGGC AGCCCCGAT CGGGAAAGCG TTTTGGGCGC GAGCGCTGGC	720
GTGCGGGTCA GTCGCTGGTG CGCAGTGCCG GGGGGAACGG GTATCGTGGG GGGCGCGGGC	780
GGAGGAGAGC GTGGCGAGGG CCGAGAGCAG CGCGCGGCCG GGTACGCAA CGCGCCCCAC	840
GTACTGCCCT CCCCCTCCGC GCGCGCTAGA AATACCGAGG CCTGGACCGG GGGGGGGCCC	900
CGTCACATCC ATCCATCGAC CGATCGATCG CCACAGCCAA CACCACCCGC CGAGGCGACG	960
CGACAGCCGC CAGGAGGAAG GAATAAACTC ACTGCCAGCC AGTGAAGGGG GAGAAGTGTA	1020
CTGCTCCGTC GACCAGTGCG CGCACCGCCC GGCAGGGCTG CTCATCTCGT CGACGACCAG	1080
GTTCTGTTCC GTTCCGATCC GATCCGATCC TGTCTTGAG TTTCGTCCAG ATCCTGGCGC	1140
GTATCTGCGT GTTTGATGAT CCAGGTTCTT CGAACCTAAA TCTGTCCGTG CACACGTCTT	1200
TTCTCTCTCT CCTACGCAGT GGATTAATCG GCATGGCGGC TCTGGCCACG TCGCAGCTCG	1260
TCGCAACGCG CGCCGGCCTG GCGTCCCGG ACGGTCCAC GTCCGCGCGC GGCGCCGCGC	1320
AGGGCCTGAG GGGGGCCCGG GCGTCGGCGG CGGCGGACAC GCTCAGCATG CGGACCAGCG	1380
CGCGCGCGGC GCCCAGGCAC CAGCAGCAGG CGCGCCGCGG GGGCAGGTTC CCGTCGCTCG	1440
TCGTGTGC GCC AGC GCC GGC ATG AAC GTC GTC TTC GTC GGC GCC GAG ATG	1490
Ala Ser Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met	
1 5 10	
GCG CCG TGG AGC AAG ACC GGC GGC CTC GGC GAC GTC CTC GGC GGC CTG	1538

Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu	
15 20 25 30	
CCG CCG GCC ATG GCC GTAAGCGCGC GCACCGAGAC ATGCATCCGT TGGATCGCGT	1593
Pro Pro Ala Met Ala	
35	
CTTCTTCGTG CTCTTGCCGC GTGCATGATG CATGTGTTTC CTCCTGGCTT GTGTTTCGTGT	1653
ATGTGACGTG TTTGTTCGGG CATGCATGCA G GCG AAC GGG CAC CGT GTC ATG	1705
Ala Asn Gly His Arg Val Met	
40	
GTC GTC TCT CCC CGC TAC GAC CAG TAC AAG GAC GCC TGG GAC ACC AGC	1753
Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr Ser	
45 50 55	
GTC GTG TCC GAG GTACGGCCAC CGAGACCAGA TTCAGATCAC AGTCACACAC	1805
Val Val Ser Glu	
60	
ACCGTCATAT GAACCTTTCT CTGCTCTGAT GCCTGCAACT GCAAATGCAT GCAG ATC	1862
Ile	
AAG ATG GGA GAC GGG TAC GAG ACG GTC AGG TTC TTC CAC TGC TAC AAG	1910
Lys Met Gly Asp Gly Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys	
65 70 75	
CGC GGA GTG GAC CGC GTG TTC GTT GAC CAC CCA CTG TTC CTG GAG AGG	1958
Arg Gly Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg	
80 85 90 95	
GTGAGACGAG ATCTGATCAC TCGATACGCA ATTACCACCC CATTGTAAGC AGTTACAGTG	2018
AGCTTTTTTTT CCCCCCGGCC TGGTCGCTGG TTTCAG GTT TGG GGA AAG ACC GAG	2072
Val Trp Gly Lys Thr Glu	
100	
GAG AAG ATC TAC GGG CCT GTC GCT GGA ACG GAC TAC AGG GAC AAC CAG	2120
Glu Lys Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln	
105 110 115	
CTG CGG TTC AGC CTG CTA TGC CAG GTCAGGATGG CTTGGTACTA CAACTTCATA	2174
Leu Arg Phe Ser Leu Leu Cys Gln	

120	125	
TCATCTGTAT GCAGCAGTAT ACACTGATGA GAAATGCATG CTGTTCTGCA G GCA GCA		2231
	Ala Ala	
CTT GAA GCT CCA AGG ATC CTG AGC CTC AAC AAC AAC CCA TAC TTC TCC		2279
Leu Glu Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser		
130	135	140
GGA CCA TAC G GTAAGAGTTG CAGTCTTCGT ATATATATCT GTTGAGCTCG		2329
Gly Pro Tyr		
145		
AGAATCTTCA CAGGAAGCGG CCCATCAGAC GGACTGTCAT TTTACACTGA CTACTGCTGC		2389
TGCTCTTCGT CCATCCATAC AAG GG GAG GAC GTC GTG TTC GTC TGC AAC		2438
Gly Glu Asp Val Val Phe Val Cys Asn		
150		155
GAC TGG CAC ACC GGC CCT CTC TCG TGC TAC CTC AAG AGC AAC TAC CAG		2486
Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys Ser Asn Tyr Gln		
160	165	170
TCC CAC GGC ATC TAC AGG GAC GCA AAG GTTGCCTTCT CTGAACTGAA		2533
Ser His Gly Ile Tyr Arg Asp Ala Lys		
175	180	
CAACGCCGTT TTCGTTCTCC ATGCTCGTAT ATACCTCGTC TGGTAGTGGT GGTGCTTCTC		2593
TGAGAAACTA ACTGAACTG ACTGCATGTC TGTCTGACCA TCTTCACGTA CTACCAG		2650
ACC GCT TTC TGC ATC CAC AAC ATC TCC TAC CAG GGC CGG TTC GCC TTC		2698
Thr Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe		
185	190	195
TCC GAC TAC CCG GAG CTG AAC CTC CCG GAG AGA TTC AAG TCG TCC TTC		2746
Ser Asp Tyr Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe		
200	205	210
GAT TTC ATC GAC GG GTCTGTTTTT CTGCGTGCA GTGAACATTC ATGAATGGTA		2800
Asp Phe Ile Asp Gly		
215		
ACCCACAACT GTTCGCGTCC TGCTGGTTCA TTATCTGACC TGATTGCATT ATTGCAG C		2858

TAC GAG AAG CCC GTG GAA GGC CGG AAG ATC AAC TGG ATG AAG GCC GGG Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly 220 225 230	2906
ATC CTC GAG GCC GAC AGG GTC CTC ACC GTC AGC CCC TAC TAC GCC GAG Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu 235 240 245	2954
GAG CTC ATC TCC GGC ATC GCC AGG GGC TGC GAG CTC GAC AAC ATC ATG Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met 250 255 260 265	3002
CGC CTC ACC GGC ATC ACC GGC ATC GTC AAC GGC ATG GAC GTC AGC GAG Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu 270 275 280	3050
TGG GAC CCC AGC AGG GAC AAG TAC ATC GCC GTG AAG TAC GAC GTG TCG Trp Asp Pro Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp Val Ser 285 290 295	3098
ACG GTGAGCTGGC TAGCTCTGAT TCTGCTGCCT GGTCTCTCTG CTCATCATGC Thr	3151
TGGTTCGGTA CTGACGCGGC AAGTGACGT ACGTGCGTGC GACGGTGGTG TCCGGTTCAG	3211
GCC GTG GAG GCC AAG GCG CTG AAC AAG GAG GCG CTG CAG GCG GAG GTC Ala Val Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln Ala Glu Val 300 305 310	3259
GGG CTC CCG GTG GAC CGG AAC ATC CCG CTG GTG GCG TTC ATC GGC AGG Gly Leu Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe Ile Gly Arg 315 320 325 330	3307
CTG GAA GAG CAG AAG GGC CCC GAC GTC ATG GCG GCC GCC ATC CCG CAG Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala Ile Pro Gln 335 340 345	3355
CTC ATG GAG ATG GTG GAG GAC GTG CAG ATC GTT CTG CTG GTACGTGTGC Leu Met Glu Met Val Glu Asp Val Gln Ile Val Leu Leu 350 355	3404
GCCGGCCGCC ACCCGGCTAC TACATGCGTG TATCGTTCGT TCTACTGGAA CATGCGTGTG	3464
AGCAACGCGA TGGATAATGC TGCAG GGC ACG GGC AAG AAG AAG TTC GAG CGC	3516

	Gly Thr Gly Lys Lys Lys Phe Glu Arg	
	360	365
ATG CTC ATG AGC GCC GAG GAG AAG TTC CCA GGC AAG GTG CGC GCC GTG		3564
Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val		
370	375	380
GTC AAG TTC AAC GCG GCG CTG GCG CAC CAC ATC ATG GCC GGC GCC GAC		3612
Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp		
385	390	395 400
GTG CTC GCC GTC ACC AGC CGC TTC GAG CCC TGC GGC CTC ATC CAG CTG		3660
Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu		
	405	410 415
CAG GGG ATG CGA TAC GGA ACG GTACGAGAGA AAAAAAAT CCTGAATCCT		3711
Gln Gly Met Arg Tyr Gly Thr		
420		
GACGAGAGGG ACAGAGACAG ATTATGAATG CTTCATCGAT TTGAATTGAT TGATCGATGT		3771
CTCCCGCTGC GACTCTTGCA G CCC TGC GCC TGC GCG TCC ACC GGT GGA CTC		3822
Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu		
425		430
GTC GAC ACC ATC ATC GAA GGC AAG ACC GGG TTC CAC ATG GGC CGC CTC		3870
Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu		
435	440	445
AGC GTC GAC GTAAGCCTAG CTCTGCCATG TTCTTTCTTC TTTCTTTCTG		3919
Ser Val Asp		
450		
TATGTATGTA TGAATCAGCA CCGCCGTTCT TGTTTCGTGC TCGTCCTCTC TTCCCAG		3976
TGT AAC GTC GTG GAG CCG GCG GAC GTC AAG AAG GTG GCC ACC ACA TTG		4024
Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala Thr Thr Leu		
455	460	465
CAG CGC GCC ATC AAG GTG GTC GGC ACG CCG GCG TAC GAG GAG ATG GTG		4072
Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val		
470	475	480
AGG AAC TGC ATG ATC CAG GAT CTC TCC TGG AAG GTACGTACGC CCGCCCCGCC		4125
Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys		

485	490	495	
CCGCCCCGCC AGAGCAGAGC GCCAAGATCG ACCGATCGAC CGACCACACG TACGCGCCTC			4185
GCTCCTGTCTG CTGACCGTGG TTTAATTTGC GAAATGCGCA G GGC CCT GCC AAG			4238
		Gly Pro Ala Lys	
AAC TGG GAG AAC GTG CTG CTC AGC CTC GGG GTC GCC GGC GGC GAG CCA			4286
Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly Glu Pro			
500	505	510	515
GGG GTC GAA GGC GAG GAG ATC GCG CCG CTC GCC AAG GAG AAC GTG GCC			4334
Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala			
	520	525	530
GCG CCC TGA AGAGTTCGGC CTGCAGGGCC CCTGATCTCG CGCGTGGTGC			4383
Ala Pro *			
AAAGATGTTG GGACATCTTC TTATATATGC TGTTTCGTTT ATGTGATATG GACAAGTATG			4443
TGTAGCTGCT TGCTTGTGCT AGTGTAATGT AGTGTAGTGG TGGCCAGTGG CACAACCTAA			4503
TAAGCGCATG AACTAATTGC TTGCGTGTGT AGTTAAGTAC CGATCGGTAA TTTTATATTG			4563
CGAGTAAATA AATGGACCTG TAGTGGTGGA GTAAATAATC CCTGCTGTTC GGTGTTCTTA			4623
TCGCTCCTCG TATAGATATT ATATAGAGTA CATTTTTCTC TCTCTGAATC CTACGTTTGT			4683
GAAATTTCTA TATCATTACT GTAAAATTTT TCGGTTCCAA AAGAGACCAT AGCCTATCTT			4743
TGGCCCTGTT TGTTTCGGCT TCTGGCAGCT TCTGGCCACC AAAAGCTGCT GCGGACT			4800

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Ser Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met Ala Pro
 1 5 10 15
 Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu Pro Pro
 20 25 30
 Ala Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr
 35 40 45
 Asp Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys
 50 55 60
 Met Gly Asp Gly Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg
 65 70 75 80
 Gly Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val
 85 90 95
 Trp Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Val Ala Gly Thr Asp
 100 105 110
 Tyr Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu
 115 120 125
 Glu Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly
 130 135 140
 Pro Tyr Gly Glu Asp Val Val Phe Val Cys Asn Asp Trp His Thr Gly
 145 150 155 160
 Pro Leu Ser Cys Tyr Leu Lys Ser Asn Tyr Gln Ser His Gly Ile Tyr
 165 170 175
 Arg Asp Ala Lys Thr Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly
 180 185 190
 Arg Phe Ala Phe Ser Asp Tyr Pro Glu Leu Asn Leu Pro Glu Arg Phe
 195 200 205
 Lys Ser Ser Phe Asp Phe Ile Asp Gly Tyr Glu Lys Pro Val Glu Gly
 210 215 220
 Arg Lys Ile Asn Trp Met Lys Ala Gly Ile Leu Glu Ala Asp Arg Val
 225 230 235 240

Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala
 245 250 255

Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly
 260 265 270

Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys
 275 280 285

Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala
 290 295 300

Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg
 305 310 315 320

Asn Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly
 325 330 335

Pro Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu
 340 345 350

Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg
 355 360 365

Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val
 370 375 380

Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
 385 390 395 400

Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu
 405 410 415

Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
 420 425 430

Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
 435 440 445

Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
 450 455 460

Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
 465 470 475 480

Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
 485 490 495

Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
 500 505 510

Gly Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu
 515 520 525

Asn Val Ala Ala Pro *
 530

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Oryza sativa

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 453..2282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCAGTG TGAAGGAATA GATTCTCTTC AAAACAATTT AATCATTCAT CTGATCTGCT	60
CAAAGCTCTG TGCATCTCCG GGTGCAACGG CCAGGATATT TATTGTGCAG TAAAAAATG	120
TCATATCCCC TAGCCACCCA AGAAACTGCT CCTTAAGTCC TTATAAGCAC ATATGGCATT	180
GTAATATATA TGTTTGAGTT TTAGCGACAA TTTTTTTAAA AACTTTTGGT CCTTTTTATG	240
AACGTTTTAA GTTTCAGTGT CTTTTTTTTT CGAATTTTAA ATGTAGCTTC AAATTCTAAT	300
CCCCAATCCA AATTGTAATA AACTTCAATT CTCCTAATTA ACATCTTAAT TCATTTATTT	360

GAAAACCAGT TCAAATTCTT TTTAGGCTCA CCAAACCTTA AACAATTCAA TTCAGTGCAG	420
AGATCTTCCA CAGCAACAGC TAGACAACCA CC ATG TCG GCT CTC ACC ACG TCC	473
Met Ser Ala Leu Thr Thr Ser	
535 540	
CAG CTC GCC ACC TCG GCC ACC GGC TTC GGC ATC GCC GAC AGG TCG GCG	521
Gln Leu Ala Thr Ser Ala Thr Gly Phe Gly Ile Ala Asp Arg Ser Ala	
545 550 555	
CCG TCG TCG CTG CTC CGC CAC GGG TTC CAG GGC CTC AAG CCC CGC AGC	569
Pro Ser Ser Leu Leu Arg His Gly Phe Gln Gly Leu Lys Pro Arg Ser	
560 565 570	
CCC GCC GGC GGC GAC GCG ACG TCG CTC AGC GTG ACG ACC AGC GCG CGC	617
Pro Ala Gly Gly Asp Ala Thr Ser Leu Ser Val Thr Thr Ser Ala Arg	
575 580 585	
GCG ACG CCC AAG CAG CAG CGG TCG GTG CAG CGT GGC AGC CGG AGG TTC	665
Ala Thr Pro Lys Gln Gln Arg Ser Val Gln Arg Gly Ser Arg Arg Phe	
590 595 600 605	
CCC TCC GTC GTC GTG TAC GCC ACC GGC GCC GGC ATG AAC GTC GTG TTC	713
Pro Ser Val Val Val Tyr Ala Thr Gly Ala Gly Met Asn Val Val Phe	
610 615 620	
GTC GGC GCC GAG ATG GCC CCC TGG AGC AAG ACC GGC GGC CTC GGT GAC	761
Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp	
625 630 635	
GTC CTC GGT GGC CTC CCC CCT GCC ATG GCT GCG AAT GGC CAC AGG GTC	809
Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His Arg Val	
640 645 650	
ATG GTG ATC TCT CCT CGG TAC GAC CAG TAC AAG GAC GCT TGG GAT ACC	857
Met Val Ile Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr	
655 660 665	
AGC GTT GTG GCT GAG ATC AAG GTT GCA GAC AGG TAC GAG AGG GTG AGG	905
Ser Val Val Ala Glu Ile Lys Val Ala Asp Arg Tyr Glu Arg Val Arg	
670 675 680 685	
TTT TTC CAT TGC TAC AAG CGT GGA GTC GAC CGT GTG TTC ATC GAC CAT	953
Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Ile Asp His	
690 695 700	

CCG TCA TTC CTG GAG AAG GTT TGG GGA AAG ACC GGT GAG AAG ATC TAC	1001
Pro Ser Phe Leu Glu Lys Val Trp Gly Lys Thr Gly Glu Lys Ile Tyr	
705 710 715	
GGA CCT GAC ACT GGA GTT GAT TAC AAA GAC AAC CAG ATG CGT TTC AGC	1049
Gly Pro Asp Thr Gly Val Asp Tyr Lys Asp Asn Gln Met Arg Phe Ser	
720 725 730	
CTT CTT TGC CAG GCA GCA CTC GAG GCT CCT AGG ATC CTA AAC CTC AAC	1097
Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Asn Leu Asn	
735 740 745	
AAC AAC CCA TAC TTC AAA GGA ACT TAT GGT GAG GAT GTT GTG TTC GTC	1145
Asn Asn Pro Tyr Phe Lys Gly Thr Tyr Gly Glu Asp Val Val Phe Val	
750 755 760 765	
TGC AAC GAC TGG CAC ACT GGC CCA CTG GCG AGC TAC CTG AAG AAC AAC	1193
Cys Asn Asp Trp His Thr Gly Pro Leu Ala Ser Tyr Leu Lys Asn Asn	
770 775 780	
TAC CAG CCC AAT GGC ATC TAC AGG AAT GCA AAG GTT GCT TTC TGC ATC	1241
Tyr Gln Pro Asn Gly Ile Tyr Arg Asn Ala Lys Val Ala Phe Cys Ile	
785 790 795	
CAC AAC ATC TCC TAC CAG GGC CGT TTC GCT TTC GAG GAT TAC CCT GAG	1289
His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Glu Asp Tyr Pro Glu	
800 805 810	
CTG AAC CTC TCC GAG AGG TTC AGG TCA TCC TTC GAT TTC ATC GAC GGG	1337
Leu Asn Leu Ser Glu Arg Phe Arg Ser Ser Phe Asp Phe Ile Asp Gly	
815 820 825	
TAT GAC ACG CCG GTG GAG GGC AGG AAG ATC AAC TGG ATG AAG GCC GGA	1385
Tyr Asp Thr Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly	
830 835 840 845	
ATC CTG GAA GCC GAC AGG GTG CTC ACC GTG AGC CCG TAC TAC GCC GAG	1433
Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu	
850 855 860	
GAG CTC ATC TCC GGC ATC GCC AGG GGA TGC GAG CTC GAC AAC ATC ATG	1481
Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met	
865 870 875	
CGG CTC ACC GGC ATC ACC GGC ATC GTC AAC GGC ATG GAC GTC AGC GAG	1529

Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu	
880 885 890	
TGG GAT CCT AGC AAG GAC AAG TAC ATC ACC GCC AAG TAC GAC GCA ACC	1577
Trp Asp Pro Ser Lys Asp Lys Tyr Ile Thr Ala Lys Tyr Asp Ala Thr	
895 900 905	
ACG GCA ATC GAG GCG AAG GCG CTG AAC AAG GAG GCG TTG CAG GCG GAG	1625
Thr Ala Ile Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln Ala Glu	
910 915 920 925	
GCG GGT CTT CCG GTC GAC AGG AAA ATC CCA CTG ATC GCG TTC ATC GGC	1673
Ala Gly Leu Pro Val Asp Arg Lys Ile Pro Leu Ile Ala Phe Ile Gly	
930 935 940	
AGG CTG GAG GAA CAG AAG GGC CCT GAC GTC ATG GCC GCC GCC ATC CCG	1721
Arg Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala Ile Pro	
945 950 955	
GAG CTC ATG CAG GAG GAC GTC CAG ATC GTT CTT CTG GGT ACT GGA AAG	1769
Glu Leu Met Gln Glu Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys	
960 965 970	
AAG AAG TTC GAG AAG CTG CTC AAG AGC ATG GAG GAG AAG TAT CCG GGC	1817
Lys Lys Phe Glu Lys Leu Leu Lys Ser Met Glu Glu Lys Tyr Pro Gly	
975 980 985	
AAG GTG AGG GCG GTG GTG AAG TTC AAC GCG CCG CTT GCT CAT CTC ATC	1865
Lys Val Arg Ala Val Val Lys Phe Asn Ala Pro Leu Ala His Leu Ile	
990 995 1000 1005	
ATG GCC GGA GCC GAC GTG CTC GCC GTC CCC AGC CGC TTC GAG CCC TGT	1913
Met Ala Gly Ala Asp Val Leu Ala Val Pro Ser Arg Phe Glu Pro Cys	
1010 1015 1020	
GGA CTC ATC CAG CTG CAG GGG ATG AGA TAC GGA ACG CCC TGT GCT TGC	1961
Gly Leu Ile Gln Leu Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys	
1025 1030 1035	
GCG TCC ACC GGT GGG CTC GTG GAC ACG GTC ATC GAA GGC AAG ACT GGT	2009
Ala Ser Thr Gly Gly Leu Val Asp Thr Val Ile Glu Gly Lys Thr Gly	
1040 1045 1050	
TTC CAC ATG GGC CGT CTC AGC GTC GAC TGC AAG GTG GTG GAG CCA AGC	2057
Phe His Met Gly Arg Leu Ser Val Asp Cys Lys Val Val Glu Pro Ser	

1055	1060	1065	
GAC GTG AAG AAG GTG GCG GCC ACC CTG AAG CGC GCC ATC AAG GTC GTC			2105
Asp Val Lys Lys Val Ala Ala Thr Leu Lys Arg Ala Ile Lys Val Val			
1070	1075	1080	1085
GGC ACG CCG GCG TAC GAG GAG ATG GTC AGG AAC TGC ATG AAC CAG GAC			2153
Gly Thr Pro Ala Tyr Glu Glu Met Val Arg Asn Cys Met Asn Gln Asp			
1090	1095	1100	
CTC TCC TGG AAG GGG CCT GCG AAG AAC TGG GAG AAT GTG CTC CTG GGC			2201
Leu Ser Trp Lys Gly Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Gly			
1105	1110	1115	
CTG GGC GTC GCC GGC AGC GCG CCG GGG ATC GAA GGC GAC GAG ATC GCG			2249
Leu Gly Val Ala Gly Ser Ala Pro Gly Ile Glu Gly Asp Glu Ile Ala			
1120	1125	1130	
CCG CTC GCC AAG GAG AAC GTG GCT GCT CCT TGA AGAGCCTGAG ATCTACATAT			2302
Pro Leu Ala Lys Glu Asn Val Ala Ala Pro *			
1135	1140		
GGAGTGATTA ATTAATATAG CAGTATATGG ATGAGAGACG AATGAACCAG TGGTTTGT			2362
TTTGTAGTGA ATTTGTAGCT ATAGCCAATT ATATAGGCTA ATAAGTTTGA TGTGTACTC			2422
TTCTGGGTGT GCTTAAGTAT CTTATCGGAC CCTGAATTTA TGTGTGTGGC TTATTGCCAA			2482
TAATATTAAG TAATAAAGGG TTTATTATAT TATTATATAT GTTATATTAT ACTAAAAAA			2542

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Ala	Leu	Thr	Thr	Ser	Gln	Leu	Ala	Thr	Ser	Ala	Thr	Gly	Phe
1				5					10					15	

Gly Ile Ala Asp Arg Ser Ala Pro Ser Ser Leu Leu Arg His Gly Phe			
20	25	30	
Gln Gly Leu Lys Pro Arg Ser Pro Ala Gly Gly Asp Ala Thr Ser Leu			
35	40	45	
Ser Val Thr Thr Ser Ala Arg Ala Thr Pro Lys Gln Gln Arg Ser Val,			
50	55	60	
Gln Arg Gly Ser Arg Arg Phe Pro Ser Val Val Val Tyr Ala Thr Gly			
65	70	75	80
Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser			
85	90	95	
Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met			
100	105	110	
Ala Ala Asn Gly His Arg Val Met Val Ile Ser Pro Arg Tyr Asp Gln			
115	120	125	
Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ala Glu Ile Lys Val Ala			
130	135	140	
Asp Arg Tyr Glu Arg Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val			
145	150	155	160
Asp Arg Val Phe Ile Asp His Pro Ser Phe Leu Glu Lys Val Trp Gly			
165	170	175	
Lys Thr Gly Glu Lys Ile Tyr Gly Pro Asp Thr Gly Val Asp Tyr Lys			
180	185	190	
Asp Asn Gln Met Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala			
195	200	205	
Pro Arg Ile Leu Asn Leu Asn Asn Asn Pro Tyr Phe Lys Gly Thr Tyr			
210	215	220	
Gly Glu Asp Val Val Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu			
225	230	235	240
Ala Ser Tyr Leu Lys Asn Asn Tyr Gln Pro Asn Gly Ile Tyr Arg Asn			
245	250	255	

Ala Lys Val	Ala Phe Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe
260	265 270
Ala Phe Glu Asp Tyr Pro Glu Leu Asn Leu Ser Glu Arg Phe Arg Ser	
275	280 285
Ser Phe Asp Phe Ile Asp Gly Tyr Asp Thr Pro Val Glu Gly Arg Lys	
290	295 300
Ile Asn Trp Met Lys Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr	
305	310 315 320
Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly	
	325 330 335
Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly Ile Val	
340	345 350
Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Lys Asp Lys Tyr Ile	
355	360 365
Thr Ala Lys Tyr Asp Ala Thr Thr Ala Ile Glu Ala Lys Ala Leu Asn	
370	375 380
Lys Glu Ala Leu Gln Ala Glu Ala Gly Leu Pro Val Asp Arg Lys Ile	
385	390 395 400
Pro Leu Ile Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro Asp	
	405 410 415
Val Met Ala Ala Ala Ile Pro Glu Leu Met Gln Glu Asp Val Gln Ile	
	420 425 430
Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Lys Leu Leu Lys Ser	
435	440 445
Met Glu Glu Lys Tyr Pro Gly Lys Val Arg Ala Val Val Lys Phe Asn	
450	455 460
Ala Pro Leu Ala His Leu Ile Met Ala Gly Ala Asp Val Leu Ala Val	
465	470 475 480
Pro Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln Gly Met Arg	
	485 490 495

Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu Val Asp Thr
500 505 510

Val Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu Ser Val Asp
515 520 525

Cys Lys Val Val Glu Pro Ser Asp Val Lys Lys Val Ala Ala Thr Leu
530 535 540

Lys Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val
545 550 555 560

Arg Asn Cys Met Asn Gln Asp Leu Ser Trp Lys Gly Pro Ala Lys Asn
565 570 575

Trp Glu Asn Val Leu Leu Gly Leu Gly Val Ala Gly Ser Ala Pro Gly
580 585 590

Ile Glu Gly Asp Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala Ala
595 600 605

Pro *
610

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCT GAG GCT GAG GCC GGG GGC AAG GAC GCG CCG CCG GAG AGG AGC GGC	48
Ala Glu Ala Glu Ala Gly Gly Lys Asp Ala Pro Pro Glu Arg Ser Gly	
615 620 625	
GAC GCC GCC AGG TTG CCC CGC GCT CGG CGC AAT GCG GTC TCC AAA CGG	96
Asp Ala Ala Arg Leu Pro Arg Ala Arg Arg Asn Ala Val Ser Lys Arg	
630 635 640	
AGG GAT CCT CTT CAG CCG GTC GGC CGG TAC GGC TCC GCG ACG GGA AAC	144
Arg Asp Pro Leu Gln Pro Val Gly Arg Tyr Gly Ser Ala Thr Gly Asn	
645 650 655	
ACG GCC AGG ACC GGC GCC GCG TCC TGC CAG AAC GCC GCA TTG GCG GAC	192
Thr Ala Arg Thr Gly Ala Ala Ser Cys Gln Asn Ala Ala Leu Ala Asp	
660 665 670	
GTT GAG ATC GTT GAG ATC AAG TCC ATC GTC GCC GCG CCG CCG ACG AGC	240
Val Glu Ile Val Glu Ile Lys Ser Ile Val Ala Ala Pro Pro Thr Ser	
675 680 685 690	
ATA GTG AAG TTC CCA GGG CGC GGG CTA CAG GAT GAT CCT TCC CTC TGG	288
Ile Val Lys Phe Pro Gly Arg Gly Leu Gln Asp Asp Pro Ser Leu Trp	
695 700 705	
GAC ATA GCA CCG GAG ACT GTC CTC CCA GCC CCG AAG CCA CTG CAT GAA	336
Asp Ile Ala Pro Glu Thr Val Leu Pro Ala Pro Lys Pro Leu His Glu	
710 715 720	
TCG CCT GCG GTT GAC GGA GAT TCA AAT GGA ATT GCA CCT CCT ACA GTT	384
Ser Pro Ala Val Asp Gly Asp Ser Asn Gly Ile Ala Pro Pro Thr Val	
725 730 735	
GAG CCA TTA GTA CAG GAG GCC ACT TGG GAT TTC AAG AAA TAC ATC GGT	432
Glu Pro Leu Val Gln Glu Ala Thr Trp Asp Phe Lys Lys Tyr Ile Gly	
740 745 750	
TTT GAC GAG CCT GAC GAA GCG AAG GAT GAT TCC AGG GTT GGT GCA GAT	480
Phe Asp Glu Pro Asp Glu Ala Lys Asp Asp Ser Arg Val Gly Ala Asp	
755 760 765 770	
GAT GCT GGT TCT TTT GAA CAT TAT GGG ACA ATG ATT CTG GGC CTT TGT	528
Asp Ala Gly Ser Phe Glu His Tyr Gly Thr Met Ile Leu Gly Leu Cys	
775 780 785	
GGG GAG AAT GTT ATG AAC GTG ATC GTG GTG GCT GCT GAA TGT TCT CCA	576

Gly Glu Asn Val Met Asn Val Ile Val Val Ala Ala Glu Cys Ser Pro	
790 795 800	
TGG TGC AAA ACA GGT GGT CTT GGA GAT GTT GTG GGA GCT TTA CCC AAG	624
Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Val Gly Ala Leu Pro Lys	
805 810 815	
GCT TTA GCG AGA AGA GGA CAT CGT GTT ATG GTT GTG GTA CCA AGG TAT	672
Ala Leu Ala Arg Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr	
820 825 830	
GGG GAC TAT GTG GAA GCC TTT GAT ATG GGA ATC CGG AAA TAC TAC AAA	720
Gly Asp Tyr Val Glu Ala Phe Asp Met Gly Ile Arg Lys Tyr Tyr Lys	
835 840 845 850	
GCT GCA GGA CAG GAC CTA GAA GTG AAC TAT TTC CAT GCA TTT ATT GAT	768
Ala Ala Gly Gln Asp Leu Glu Val Asn Tyr Phe His Ala Phe Ile Asp	
855 860 865	
GGA GTC GAC TTT GTG TTC ATT GAT GCC TCT TTC CGG CAC CGT CAA GAT	816
Gly Val Asp Phe Val Phe Ile Asp Ala Ser Phe Arg His Arg Gln Asp	
870 875 880	
GAC ATA TAT GGG GGA AGT AGG CAG GAA ATC ATG AAG CGC ATG ATT TTG	864
Asp Ile Tyr Gly Gly Ser Arg Gln Glu Ile Met Lys Arg Met Ile Leu	
885 890 895	
TTT TGC AAG GTT GCT GTT GAG GTT CCT TGG CAC GTT CCA TGC GGT GGT	912
Phe Cys Lys Val Ala Val Glu Val Pro Trp His Val Pro Cys Gly Gly	
900 905 910	
GTG TGC TAC GGA GAT GGA AAT TTG GTG TTC ATT GCC ATG AAT TGG CAC	960
Val Cys Tyr Gly Asp Gly Asn Leu Val Phe Ile Ala Met Asn Trp His	
915 920 925 930	
ACT GCA CTC CTG CCT GTT TAT CTG AAG GCA TAT TAC AGA GAC CAT GGG	1008
Thr Ala Leu Leu Pro Val Tyr Leu Lys Ala Tyr Tyr Arg Asp His Gly	
935 940 945	
TTA ATG CAG TAC ACT CGC TCC GTC CTC GTC ATA CAT AAC ATC GGC CAC	1056
Leu Met Gln Tyr Thr Arg Ser Val Leu Val Ile His Asn Ile Gly His	
950 955 960	
CAG GGC CGT GGT CCT GTA CAT GAA TTC CCG TAC ATG GAC TTG CTG AAC	1104
Gln Gly Arg Gly Pro Val His Glu Phe Pro Tyr Met Asp Leu Leu Asn	

965	970	975	
ACT AAC CTT CAA CAT TTC GAG CTG TAC GAT CCC GTC GGT GGC GAG CAC			1152
Thr Asn Leu Gln His Phe Glu Leu Tyr Asp Pro Val Gly Gly Glu His			
980	985	990	
GCC AAC ATC TTT GCC GCG TGT GTT CTG AAG ATG GCA GAC CGG GTG GTG			1200
Ala Asn Ile Phe Ala Ala Cys Val Leu Lys Met Ala Asp Arg Val Val			
995	1000	1005	1010
ACT GTC AGC CGC GGC TAC CTG TGG GAG CTG AAG ACA GTG GAA GGC GGC			1248
Thr Val Ser Arg Gly Tyr Leu Trp Glu Leu Lys Thr Val Glu Gly Gly			
1015	1020	1025	
TGG GGC CTC CAC GAC ATC ATC CGT TCT AAC GAC TGG AAG ATC AAT GGC			1296
Trp Gly Leu His Asp Ile Ile Arg Ser Asn Asp Trp Lys Ile Asn Gly			
1030	1035	1040	
ATT CGT GAA CGC ATC GAC CAC CAG GAG TGG AAC CCC AAG GTG GAC GTG			1344
Ile Arg Glu Arg Ile Asp His Gln Glu Trp Asn Pro Lys Val Asp Val			
1045	1050	1055	
CAC CTG CGG TCG GAC GGC TAC ACC AAC TAC TCC CTC GAG ACA CTC GAC			1392
His Leu Arg Ser Asp Gly Tyr Thr Asn Tyr Ser Leu Glu Thr Leu Asp			
1060	1065	1070	
GCT GGA AAG CGG CAG TGC AAG GCG GCC CTG CAG CGG GAC GTG GGC CTG			1440
Ala Gly Lys Arg Gln Cys Lys Ala Ala Leu Gln Arg Asp Val Gly Leu			
1075	1080	1085	1090
GAA GTG CGC GAC GAC GTG CCG CTG CTC GGC TTC ATC GGG CGT CTG GAT			1488
Glu Val Arg Asp Asp Val Pro Leu Leu Gly Phe Ile Gly Arg Leu Asp			
1095	1100	1105	
GGA CAG AAG GGC GTG GAC ATC ATC GGG GAC GCG ATG CCG TGG ATC GCG			1536
Gly Gln Lys Gly Val Asp Ile Ile Gly Asp Ala Met Pro Trp Ile Ala			
1110	1115	1120	
GGG CAG GAC GTG CAG CTG GTG ATG CTG GGC ACC GGC CCA CCT GAC CTG			1584
Gly Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Pro Pro Asp Leu			
1125	1130	1135	
GAA CGA ATG CTG CAG CAC TTG GAG CGG GAG CAT CCC AAC AAG GTG CGC			1632
Glu Arg Met Leu Gln His Leu Glu Arg Glu His Pro Asn Lys Val Arg			
1140	1145	1150	

1	5	10	15
Asp Ala Ala Arg Leu Pro Arg Ala Arg Arg Asn Ala Val Ser Lys Arg			
20	25	30	
Arg Asp Pro Leu Gln Pro Val Gly Arg Tyr Gly Ser Ala Thr Gly Asn			
35	40	45	
Thr Ala Arg Thr Gly Ala Ala Ser Cys Gln Asn Ala Ala Leu Ala Asp			
50	55	60	
Val Glu Ile Val Glu Ile Lys Ser Ile Val Ala Ala Pro Pro Thr Ser			
65	70	75	80
Ile Val Lys Phe Pro Gly Arg Gly Leu Gln Asp Asp Pro Ser Leu Trp			
85	90	95	
Asp Ile Ala Pro Glu Thr Val Leu Pro Ala Pro Lys Pro Leu His Glu			
100	105	110	
Ser Pro Ala Val Asp Gly Asp Ser Asn Gly Ile Ala Pro Pro Thr Val			
115	120	125	
Glu Pro Leu Val Gln Glu Ala Thr Trp Asp Phe Lys Lys Tyr Ile Gly			
130	135	140	
Phe Asp Glu Pro Asp Glu Ala Lys Asp Asp Ser Arg Val Gly Ala Asp			
145	150	155	160
Asp Ala Gly Ser Phe Glu His Tyr Gly Thr Met Ile Leu Gly Leu Cys			
165	170	175	
Gly Glu Asn Val Met Asn Val Ile Val Val Ala Ala Glu Cys Ser Pro			
180	185	190	
Trp Cys Lys Thr Gly Gly Leu Gly Asp Val Val Gly Ala Leu Pro Lys			
195	200	205	
Ala Leu Ala Arg Arg Gly His Arg Val Met Val Val Val Pro Arg Tyr			
210	215	220	
Gly Asp Tyr Val Glu Ala Phe Asp Met Gly Ile Arg Lys Tyr Tyr Lys			
225	230	235	240
Ala Ala Gly Gln Asp Leu Glu Val Asn Tyr Phe His Ala Phe Ile Asp			

245							250							255													
Gly	Val	Asp	Phe	Val	Phe	Ile	Asp	Ala	Ser	Phe	Arg	His	Arg	Gln	Asp												
			260					265					270														
Asp	Ile	Tyr	Gly	Gly	Ser	Arg	Gln	Glu	Ile	Met	Lys	Arg	Met	Ile	Leu												
		275					280					285															
Phe	Cys	Lys	Val	Ala	Val	Glu	Val	Pro	Trp	His	Val	Pro	Cys	Gly	Gly												
		290				295					300																
Val	Cys	Tyr	Gly	Asp	Gly	Asn	Leu	Val	Phe	Ile	Ala	Met	Asn	Trp	His												
305					310					315					320												
Thr	Ala	Leu	Leu	Pro	Val	Tyr	Leu	Lys	Ala	Tyr	Tyr	Arg	Asp	His	Gly												
				325				330						335													
Leu	Met	Gln	Tyr	Thr	Arg	Ser	Val	Leu	Val	Ile	His	Asn	Ile	Gly	His												
			340					345					350														
Gln	Gly	Arg	Gly	Pro	Val	His	Glu	Phe	Pro	Tyr	Met	Asp	Leu	Leu	Asn												
		355					360					365															
Thr	Asn	Leu	Gln	His	Phe	Glu	Leu	Tyr	Asp	Pro	Val	Gly	Gly	Glu	His												
	370					375					380																
Ala	Asn	Ile	Phe	Ala	Ala	Cys	Val	Leu	Lys	Met	Ala	Asp	Arg	Val	Val												
385					390					395					400												
Thr	Val	Ser	Arg	Gly	Tyr	Leu	Trp	Glu	Leu	Lys	Thr	Val	Glu	Gly	Gly												
				405				410						415													
Trp	Gly	Leu	His	Asp	Ile	Ile	Arg	Ser	Asn	Asp	Trp	Lys	Ile	Asn	Gly												
			420					425					430														
Ile	Arg	Glu	Arg	Ile	Asp	His	Gln	Glu	Trp	Asn	Pro	Lys	Val	Asp	Val												
		435					440					445															
His	Leu	Arg	Ser	Asp	Gly	Tyr	Thr	Asn	Tyr	Ser	Leu	Glu	Thr	Leu	Asp												
	450					455					460																
Ala	Gly	Lys	Arg	Gln	Cys	Lys	Ala	Ala	Leu	Gln	Arg	Asp	Val	Gly	Leu												
465					470					475					480												
Glu	Val	Arg	Asp	Asp	Val	Pro	Leu	Leu	Gly</																		

Gly Val Asp Phe Val Phe Ile Asp Ala Ser Phe Arg His Arg Gln Asp
260 265 270

485	490	495
Gly Gln Lys Gly Val Asp Ile Ile Gly Asp Ala Met Pro Trp Ile Ala		
500	505	510
Gly Gln Asp Val Gln Leu Val Met Leu Gly Thr Gly Pro Pro Asp Leu		
515	520	525
Glu Arg Met Leu Gln His Leu Glu Arg Glu His Pro Asn Lys Val Arg		
530	535	540
Gly Trp Val Gly Phe Ser Val Leu Met Val His Arg Ile Thr Pro Gly		
545	550	555
Ala Ser Val Leu Val Met Pro Ser Arg Phe Ala Gly Gly Leu Asn Gln		
565	570	575
Leu Tyr Ala Met Ala Tyr Gly Thr Val Pro Val Val His Ala Val Gly		
580	585	590
Gly Leu Arg Asp Thr Val Ala Pro Phe Asp Pro Phe Gly Asp Ala Gly		
595	600	605
Leu Gly Trp Thr Phe Asp Arg Ala Glu Ala Asn Lys Leu Ile Glu Val		
610	615	620
Leu Ser His Cys Leu Asp Thr Tyr Arg Asn Tyr Glu Glu Ser Trp Lys		
625	630	635
Ser Leu Gln Ala Arg Gly Met Ser Gln Asn Leu Ser Trp Asp His Ala		
645	650	655
Ala Glu Leu Tyr Glu Asp Val Leu Val Lys Tyr Gln Trp		
660	665	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2097 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG CCG GGG GCA ATC TCT TCC TCG TCG TCG GCT TTT CTC CTC CCC GTC	48
Met Pro Gly Ala Ile Ser Ser Ser Ser Ser Ala Phe Leu Leu Pro Val	
670 675 680 685	
GCG TCC TCC TCG CCG CGG CGC AGG CGG GGC AGT GTG GGT GCT GCT CTG	96
Ala Ser Ser Ser Pro Arg Arg Arg Arg Gly Ser Val Gly Ala Ala Leu	
690 695 700	
CGC TCG TAC GGC TAC AGC GGC GCG GAG CTG CGG TTG CAT TGG GCG CGG	144
Arg Ser Tyr Gly Tyr Ser Gly Ala Glu Leu Arg Leu His Trp Ala Arg	
705 710 715	
CGG GGC CCG CCT CAG GAT GGA GCG GCG TCG GTA CGC GCC GCA GCG GCA	192
Arg Gly Pro Pro Gln Asp Gly Ala Ala Ser Val Arg Ala Ala Ala Ala	
720 725 730	
CCG GCC GGG GGC GAA AGC GAG GAG GCA GCG AAG AGC TCC TCC TCG TCC	240
Pro Ala Gly Gly Glu Ser Glu Glu Ala Ala Lys Ser Ser Ser Ser Ser	
735 740 745	
CAG GCG GGC GCT GTT CAG GGC AGC ACG GCC AAG GCT GTG GAT TCT GCT	288
Gln Ala Gly Ala Val Gln Gly Ser Thr Ala Lys Ala Val Asp Ser Ala	
750 755 760 765	
TCA CCT CCC AAT CCT TTG ACA TCT GCT CCG AAG CAA AGT CAG AGC GCT	336
Ser Pro Pro Asn Pro Leu Thr Ser Ala Pro Lys Gln Ser Gln Ser Ala	
770 775 780	
GCA ATG CAA AAC GGA ACG AGT GGG GGC AGC AGC GCG AGC ACC GCC GCG	384
Ala Met Gln Asn Gly Thr Ser Gly Gly Ser Ser Ala Ser Thr Ala Ala	
785 790 795	
CCG GTG TCC GGA CCC AAA GCT GAT CAT CCA TCA GCT CCT GTC ACC AAG	432

Pro Val Ser Gly Pro Lys Ala Asp His Pro Ser Ala Pro Val Thr Lys	
800 805 810	
AGA GAA ATC GAT GCC AGT GCG GTG AAG CCA GAG CCC GCA GGT GAT GAT	480
Arg Glu Ile Asp Ala Ser Ala Val Lys Pro Glu Pro Ala Gly Asp Asp	
815 820 825	
GCT AGA CCG GTG GAA AGC ATA GGC ATC GCT GAA CCG GTG GAT GCT AAG	528
Ala Arg Pro Val Glu Ser Ile Gly Ile Ala Glu Pro Val Asp Ala Lys	
830 835 840 845	
GCT GAT GCA GCT CCG GCT ACA GAT GCG GCG GCG AGT GCT CCT TAT GAC	576
Ala Asp Ala Ala Pro Ala Thr Asp Ala Ala Ala Ser Ala Pro Tyr Asp	
850 855 860	
AGG GAG GAT AAT GAA CCT GGC CCT TTG GCT GGG CCT AAT GTG ATG AAC	624
Arg Glu Asp Asn Glu Pro Gly Pro Leu Ala Gly Pro Asn Val Met Asn	
865 870 875	
GTC GTC GTG GTG GCT TCT GAA TGT GCT CCT TTC TGC AAG ACA GGT GGC	672
Val Val Val Val Ala Ser Glu Cys Ala Pro Phe Cys Lys Thr Gly Gly	
880 885 890	
CTT GGA GAT GTC GTG GGT GCT TTG CCT AAG GCT CTG GCG AGG AGA GGA	720
Leu Gly Asp Val Val Gly Ala Leu Pro Lys Ala Leu Ala Arg Arg Gly	
895 900 905	
CAC CGT GTT ATG GTC GTG ATA CCA AGA TAT GGA GAG TAT GCC GAA GCC	768
His Arg Val Met Val Val Ile Pro Arg Tyr Gly Glu Tyr Ala Glu Ala	
910 915 920 925	
CGG GAT TTA GGT GTA AGG AGA CGT TAC AAG GTA GCT GGA CAG GAT TCA	816
Arg Asp Leu Gly Val Arg Arg Arg Tyr Lys Val Ala Gly Gln Asp Ser	
930 935 940	
GAA GTT ACT TAT TTT CAC TCT TAC ATT GAT GGA GTT GAT TTT GTA TTC	864
Glu Val Thr Tyr Phe His Ser Tyr Ile Asp Gly Val Asp Phe Val Phe	
945 950 955	
GTA GAA GCC CCT CCC TTC CGG CAC CGG CAC AAT AAT ATT TAT GGG GGA	912
Val Glu Ala Pro Pro Phe Arg His Arg His Asn Asn Ile Tyr Gly Gly	
960 965 970	
GAA AGA TTG GAT ATT TTG AAG CGC ATG ATT TTG TTC TGC AAG GCC GCT	960
Glu Arg Leu Asp Ile Leu Lys Arg Met Ile Leu Phe Cys Lys Ala Ala	

975	980	985	
GTT GAG GTT CCA TGG TAT GCT CCA TGT GGC GGT ACT GTC TAT GGT GAT			1008
Val Glu Val Pro Trp Tyr Ala Pro Cys Gly Gly Thr Val Tyr Gly Asp			
990	995	1000	1005
GGC AAC TTA GTT TTC ATT GCT AAT GAT TGG CAT ACC GCA CTT CTG CCT			1056
Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro			
	1010	1015	1020
GTC TAT CTA AAG GCC TAT TAC CGG GAC AAT GGT TTG ATG CAG TAT GCT			1104
Val Tyr Leu Lys Ala Tyr Tyr Arg Asp Asn Gly Leu Met Gln Tyr Ala			
	1025	1030	1035
CGC TCT GTG CTT GTG ATA CAC AAC ATT GCT CAT CAG GGT CGT GGC CCT			1152
Arg Ser Val Leu Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro			
	1040	1045	1050
GTA GAC GAC TTC GTC AAT TTT GAC TTG CCT GAA CAC TAC ATC GAC CAC			1200
Val Asp Asp Phe Val Asn Phe Asp Leu Pro Glu His Tyr Ile Asp His			
	1055	1060	1065
TTC AAA CTG TAT GAC AAC ATT GGT GGG GAT CAC AGC AAC GTT TTT GCT			1248
Phe Lys Leu Tyr Asp Asn Ile Gly Gly Asp His Ser Asn Val Phe Ala			
1070	1075	1080	1085
GCG GGG CTG AAG ACG GCA GAC CGG GTG GTG ACC GTT AGC AAT GGC TAC			1296
Ala Gly Leu Lys Thr Ala Asp Arg Val Val Thr Val Ser Asn Gly Tyr			
	1090	1095	1100
ATG TGG GAG CTG AAG ACT TCG GAA GGC GGG TGG GGC CTC CAC GAC ATC			1344
Met Trp Glu Leu Lys Thr Ser Glu Gly Gly Trp Gly Leu His Asp Ile			
	1105	1110	1115
ATA AAC CAG AAC GAC TGG AAG CTG CAG GGC ATC GTG AAC GGC ATC GAC			1392
Ile Asn Gln Asn Asp Trp Lys Leu Gln Gly Ile Val Asn Gly Ile Asp			
	1120	1125	1130
ATG AGC GAG TGG AAC CCC GCT GTG GAC GTG CAC CTC CAC TCC GAC GAC			1440
Met Ser Glu Trp Asn Pro Ala Val Asp Val His Leu His Ser Asp Asp			
	1135	1140	1145
TAC ACC AAC TAC ACG TTC GAG ACG CTG GAC ACC GGC AAG CGG CAG TGC			1488
Tyr Thr Asn Tyr Thr Phe Glu Thr Leu Asp Thr Gly Lys Arg Gln Cys			
1150	1155	1160	1165

AAG GCC GCC CTG CAG CGG CAG CTG GAG CTG CAG GTC CGC GAC GAC GTG	1536
Lys Ala Ala Leu Gln Arg Gln Leu Gly Leu Gln Val Arg Asp Asp Val	
1170 1175 1180	
CCA CTG ATC GGG TTC ATC GGG CGG CTG GAC CAC CAG AAG GAG GTG GAC	1584
Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp His Gln Lys Gly Val Asp	
1185 1190 1195	
ATC ATC GCC GAC GCG ATC CAC TGG ATC GCG GGG CAG GAC GTG CAG CTC	1632
Ile Ile Ala Asp Ala Ile His Trp Ile Ala Gly Gln Asp Val Gln Leu	
1200 1205 1210	
GTG ATG CTG GGC ACC GGG CGG GCC GAC CTG GAG GAC ATG CTG CGG CGG	1680
Val Met Leu Gly Thr Gly Arg Ala Asp Leu Glu Asp Met Leu Arg Arg	
1215 1220 1225	
TTC GAG TCG GAG CAC AGC GAC AAG GTG CGC GCG TGG GTG GGG TTC TCG	1728
Phe Glu Ser Glu His Ser Asp Lys Val Arg Ala Trp Val Gly Phe Ser	
1230 1235 1240 1245	
GTG CCC CTG GCG CAC CGC ATC ACG GCG GGC GCG GAC ATC CTG CTG ATG	1776
Val Pro Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ile Leu Leu Met	
1250 1255 1260	
CCG TCG CGG TTC GAG CCG TGC GGG CTG AAC CAG CTC TAC GCC ATG GCG	1824
Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala	
1265 1270 1275	
TAC GGG ACC GTG CCC GTG GTG CAC GCC GTG GGG GGG CTC CGG GAC ACG	1872
Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu Arg Asp Thr	
1280 1285 1290	
GTG GCG CCG TTC GAC CCG TTC AAC GAC ACC GGG CTC GGG TGG ACG TTC	1920
Val Ala Pro Phe Asp Pro Phe Asn Asp Thr Gly Leu Gly Trp Thr Phe	
1295 1300 1305	
GAC CGC GCG GAG GCG AAC CGG ATG ATC GAC GCG CTC TCG CAC TGC CTC	1968
Asp Arg Ala Glu Ala Asn Arg Met Ile Asp Ala Leu Ser His Cys Leu	
1310 1315 1320 1325	
ACC ACG TAC CGG AAC TAC AAG GAG AGC TGG CGC GCC TGC AGG GCG CGC	2016
Thr Thr Tyr Arg Asn Tyr Lys Glu Ser Trp Arg Ala Cys Arg Ala Arg	
1330 1335 1340	
GGC ATG GCC GAG GAC CTC AGC TGG GAC CAC GCC GCC GTG CTG TAT GAG	2064

Gly Met Ala Glu Asp Leu Ser Trp Asp His Ala Ala Val Leu Tyr Glu
1345 1350 1355

GAC GTG CTC GTC AAG GCG AAG TAC CAG TGG TGA
Asp Val Leu Val Lys Ala Lys Tyr Gln Trp *
1360 1365

2097

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Gly Ala Ile Ser Ser Ser Ser Ser Ala Phe Leu Leu Pro Val
1 5 10 15

Ala Ser Ser Ser Pro Arg Arg Arg Arg Gly Ser Val Gly Ala Ala Leu
20 25 30

Arg Ser Tyr Gly Tyr Ser Gly Ala Glu Leu Arg Leu His Trp Ala Arg
35 40 45

Arg Gly Pro Pro Gln Asp Gly Ala Ala Ser Val Arg Ala Ala Ala Ala
50 55 60

Pro Ala Gly Gly Glu Ser Glu Glu Ala Ala Lys Ser Ser Ser Ser Ser
65 70 75 80

Gln Ala Gly Ala Val Gln Gly Ser Thr Ala Lys Ala Val Asp Ser Ala
85 90 95

Ser Pro Pro Asn Pro Leu Thr Ser Ala Pro Lys Gln Ser Gln Ser Ala
100 105 110

Ala Met Gln Asn Gly Thr Ser Gly Gly Ser Ser Ala Ser Thr Ala Ala
115 120 125

Pro Val Ser Gly Pro Lys Ala Asp His Pro Ser Ala Pro Val Thr Lys
130 135 140

Arg Glu Ile Asp Ala Ser Ala Val Lys Pro Glu Pro Ala Gly Asp Asp
 145 150 155 160

Ala Arg Pro Val Glu Ser Ile Gly Ile Ala Glu Pro Val Asp Ala Lys
 165 170 175

Ala Asp Ala Ala Pro Ala Thr Asp Ala Ala Ala Ser Ala Pro Tyr Asp
 180 185 190

Arg Glu Asp Asn Glu Pro Gly Pro Leu Ala Gly Pro Asn Val Met Asn
 195 200 205

Val Val Val Val Ala Ser Glu Cys Ala Pro Phe Cys Lys Thr Gly Gly
 210 215 220

Leu Gly Asp Val Val Gly Ala Leu Pro Lys Ala Leu Ala Arg Arg Gly
 225 230 235 240

His Arg Val Met Val Val Ile Pro Arg Tyr Gly Glu Tyr Ala Glu Ala
 245 250 255

Arg Asp Leu Gly Val Arg Arg Arg Tyr Lys Val Ala Gly Gln Asp Ser
 260 265 270

Glu Val Thr Tyr Phe His Ser Tyr Ile Asp Gly Val Asp Phe Val Phe
 275 280 285

Val Glu Ala Pro Pro Phe Arg His Arg His Asn Asn Ile Tyr Gly Gly
 290 295 300

Glu Arg Leu Asp Ile Leu Lys Arg Met Ile Leu Phe Cys Lys Ala Ala
 305 310 315 320

Val Glu Val Pro Trp Tyr Ala Pro Cys Gly Gly Thr Val Tyr Gly Asp
 325 330 335

Gly Asn Leu Val Phe Ile Ala Asn Asp Trp His Thr Ala Leu Leu Pro
 340 345 350

Val Tyr Leu Lys Ala Tyr Tyr Arg Asp Asn Gly Leu Met Gln Tyr Ala
 355 360 365

Arg Ser Val Leu Val Ile His Asn Ile Ala His Gln Gly Arg Gly Pro
 370 375 380

Val Asp Asp Phe Val Asn Phe Asp Leu Pro Glu His Tyr Ile Asp His			
385	390	395	400
Phe Lys Leu Tyr Asp Asn Ile Gly Gly Asp His Ser Asn Val Phe Ala			
	405	410	415
Ala Gly Leu Lys Thr Ala Asp Arg Val Val Thr Val Ser Asn Gly Tyr			
	420	425	430
Met Trp Glu Leu Lys Thr Ser Glu Gly Gly Trp Gly Leu His Asp Ile			
	435	440	445
Ile Asn Gln Asn Asp Trp Lys Leu Gln Gly Ile Val Asn Gly Ile Asp			
	450	455	460
Met Ser Glu Trp Asn Pro Ala Val Asp Val His Leu His Ser Asp Asp			
	465	470	475
Tyr Thr Asn Tyr Thr Phe Glu Thr Leu Asp Thr Gly Lys Arg Gln Cys			
	485	490	495
Lys Ala Ala Leu Gln Arg Gln Leu Gly Leu Gln Val Arg Asp Asp Val			
	500	505	510
Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp His Gln Lys Gly Val Asp			
	515	520	525
Ile Ile Ala Asp Ala Ile His Trp Ile Ala Gly Gln Asp Val Gln Leu			
	530	535	540
Val Met Leu Gly Thr Gly Arg Ala Asp Leu Glu Asp Met Leu Arg Arg			
	545	550	555
Phe Glu Ser Glu His Ser Asp Lys Val Arg Ala Trp Val Gly Phe Ser			
	565	570	575
Val Pro Leu Ala His Arg Ile Thr Ala Gly Ala Asp Ile Leu Leu Met			
	580	585	590
Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Ala			
	595	600	605
Tyr Gly Thr Val Pro Val Val His Ala Val Gly Gly Leu Arg Asp Thr			
	610	615	620

Val Ala Pro Phe Asp Pro Phe Asn Asp Thr Gly Leu Gly Trp Thr Phe
625 630 635 640

Asp Arg Ala Glu Ala Asn Arg Met Ile Asp Ala Leu Ser His Cys Leu
645 650 655

Thr Thr Tyr Arg Asn Tyr Lys Glu Ser Trp Arg Ala Cys Arg Ala Arg
660 665 670

Gly Met Ala Glu Asp Leu Ser Trp Asp His Ala Ala Val Leu Tyr Glu
675 680 685

Asp Val Leu Val Lys Ala Lys Tyr Gln Trp *
690 695

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGC GTC GCG GAG CTG AGC AGG GAG GGG CCC GCG CCG CGC CCG CTG CCA 48
Cys Val Ala Glu Leu Ser Arg Glu Gly Pro Ala Pro Arg Pro Leu Pro
700 705 710 715

CCC GCG CTG CTG GCG CCC CCG CTC GTG CCC GGC TTC CTC GCG CCG CCG 96
Pro Ala Leu Leu Ala Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro
720 725 730

GCC GAG CCC ACG GGT GAG CCG GCA TCG ACG CCG CCG CCC GTG CCC GAC	144
Ala Glu Pro Thr Gly Glu Pro Ala Ser Thr Pro Pro Pro Val Pro Asp	
735 740 745	
GCC GGC CTG GGG GAC CTC GGT CTC GAA CCT GAA GGG ATT GCT GAA GGT	192
Ala Gly Leu Gly Asp Leu Gly Leu Glu Pro Glu Gly Ile Ala Glu Gly	
750 755 760	
TCC ATC GAT AAC ACA GTA GTT GTG GCA AGT GAG CAA GAT TCT GAG ATT	240
Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln Asp Ser Glu Ile	
765 770 775	
GTG GTT GGA AAG GAG CAA GCT CGA GCT AAA GTA ACA CAA AGC ATT GTC	288
Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr Gln Ser Ile Val	
780 785 790 795	
TTT GTA ACC GGC GAA GCT TCT CCT TAT GCA AAG TCT GGG GGT CTA GGA	336
Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser Gly Gly Leu Gly	
800 805 810	
GAT GTT TGT GGT TCA TTG CCA GTT GCT CTT GCT GCT CGT GGT CAC CGT	384
Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala Arg Gly His Arg	
815 820 825	
GTG ATG GTT GTA ATG CCC AGA TAT TTA AAT GGT ACC TCC GAT AAG AAT	432
Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr Ser Asp Lys Asn	
830 835 840	
TAT GCA AAT GCA TTT TAC ACA GAA AAA CAC ATT CGG ATT CCA TGC TTT	480
Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg Ile Pro Cys Phe	
845 850 855	
GGC GGT GAA CAT GAA GTT ACC TTC TTC CAT GAG TAT AGA GAT TCA GTT	528
Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Ser Val	
860 865 870 875	
GAC TGG GTG TTT GTT GAT CAT CCC TCA TAT CAC AGA CCT GGA AAT TTA	576
Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Asn Leu	
880 885 890	
TAT GGA GAT AAG TTT GGT GCT TTT GGT GAT AAT CAG TTC AGA TAC ACA	624
Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr	
895 900 905	
CTC CTT TGC TAT GCT GCA TGT GAG GCT CCT TTG ATC CTT GAA TTG GGA	672

Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly	
910 915 920	
GGA TAT ATT TAT GGA CAG AAT TGC ATG TTT GTT GTC AAT GAT TGG CAT	720
Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His	
925 930 935	
GCC AGT CTA GTG CCA GTC CTT CTT GCT GCA AAA TAT AGA CCA TAT GGT	768
Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly	
940 945 950 955	
GTT TAT AAA GAC TCC CGC AGC ATT CTT GTA ATA CAT AAT TTA GCA CAT	816
Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His Asn Leu Ala His	
960 965 970	
CAG GGT GTA GAG CCT GCA AGC ACA TAT CCT GAC CTT GGG TTG CCA CCT	864
Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro	
975 980 985	
GAA TGG TAT GGA GCT CTG GAG TGG GTA TTC CCT GAA TGG GCG AGG AGG	912
Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg	
990 995 1000	
CAT GCC CTT GAC AAG GGT GAG GCA GTT AAT TTT TTG AAA GGT GCA GTT	960
His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val	
1005 1010 1015	
GTG ACA GCA GAT CGA ATC GTG ACT GTC AGT AAG GGT TAT TCG TGG GAG	1008
Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly Tyr Ser Trp Glu	
1020 1025 1030 1035	
GTC ACA ACT GCT GAA GGT GGA CAG GGC CTC AAT GAG CTC TTA AGC TCC	1056
Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser	
1040 1045 1050	
AGA AAG AGT GTA TTA AAC GGA ATT GTA AAT GGA ATT GAC ATT AAT GAT	1104
Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp	
1055 1060 1065	
TGG AAC CCT GCC ACA GAC AAA TGT ATC CCC TGT CAT TAT TCT GTT GAT	1152
Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His Tyr Ser Val Asp	
1070 1075 1080	
GAC CTC TCT GGA AAG GCC AAA TGT AAA GGT GCA TTG CAG AAG GAG CTG	1200
Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu Gln Lys Glu Leu	

1085	1090	1095	
GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC TTT ATT GGA AGG			1248
Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly Phe Ile Gly Arg			
1100	1105	1110	1115
TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT ATC ATA CCA GAT			1296
Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu Ile Ile Pro Asp			
	1120	1125	1130
CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA TCT GGT GAC CCA			1344
Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro			
	1135	1140	1145
GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC TTC AAG GAT AAA			1392
Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile Phe Lys Asp Lys			
	1150	1155	1160
TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC CAC CGA ATA ACT			1440
Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr			
	1165	1170	1175
GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC GAA CCT TGT GGT			1488
Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly			
1180	1185	1190	1195
CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT CCT GTT GTC CAT			1536
Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His			
	1200	1205	1210
GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC AAC CCT TTC GGT			1584
Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe Asn Pro Phe Gly			
	1215	1220	1225
GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA CCC CTA ACC ACA			1632
Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala Pro Leu Thr Thr			
	1230	1235	1240
GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC TAC ATA CAG GGA			1680
Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile Tyr Ile Gln Gly			
1245	1250	1255	
ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG CAT GTC AAA AGA			1728
Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg His Val Lys Arg			
1260	1265	1270	1275

CTT CAC GTG GGA CCA TGC CGC TGA
 Leu His Val Gly Pro Cys Arg *
 1280

1752

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys	Val	Ala	Glu	Leu	Ser	Arg	Glu	Gly	Pro	Ala	Pro	Arg	Pro	Leu	Pro	1	5	10	15
Pro	Ala	Leu	Leu	Ala	Pro	Pro	Leu	Val	Pro	Gly	Phe	Leu	Ala	Pro	Pro	20	25	30	
Ala	Glu	Pro	Thr	Gly	Glu	Pro	Ala	Ser	Thr	Pro	Pro	Pro	Val	Pro	Asp	35	40	45	
Ala	Gly	Leu	Gly	Asp	Leu	Gly	Leu	Glu	Pro	Glu	Gly	Ile	Ala	Glu	Gly	50	55	60	
Ser	Ile	Asp	Asn	Thr	Val	Val	Val	Ala	Ser	Glu	Gln	Asp	Ser	Glu	Ile	65	70	75	80
Val	Val	Gly	Lys	Glu	Gln	Ala	Arg	Ala	Lys	Val	Thr	Gln	Ser	Ile	Val	85	90	95	
Phe	Val	Thr	Gly	Glu	Ala	Ser	Pro	Tyr	Ala	Lys	Ser	Gly	Gly	Leu	Gly	100	105	110	
Asp	Val	Cys	Gly	Ser	Leu	Pro	Val	Ala	Leu	Ala	Ala	Arg	Gly	His	Arg	115	120	125	
Val	Met	Val	Val	Met	Pro	Arg	Tyr	Leu	Asn	Gly	Thr	Ser	Asp	Lys	Asn	130	135	140	
Tyr	Ala	Asn	Ala	Phe	Tyr	Thr	Glu	Lys	His	Ile	Arg	Ile	Pro	Cys	Phe	145	150	155	160

Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Ser Val			
165	170	175	
Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Asn Leu			
180	185	190	
Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr			
195	200	205	
Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly			
210	215	220	
Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His			
225	230	235	240
Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly			
245	250	255	
Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His Asn Leu Ala His			
260	265	270	
Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro			
275	280	285	
Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg			
290	295	300	
His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val			
305	310	315	320
Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly Tyr Ser Trp Glu			
325	330	335	
Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser			
340	345	350	
Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp			
355	360	365	
Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His Tyr Ser Val Asp			
370	375	380	
Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu Gln Lys Glu Leu			
385	390	395	400

Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly Phe Ile Gly Arg
405 410 415

Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu Ile Ile Pro Asp
420 425 430

Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro
435 440 445

Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile Phe Lys Asp Lys
450 455 460

Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr
465 470 475 480

Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe Glu Pro Cys Gly
485 490 495

Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val Pro Val Val His
500 505 510

Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe Asn Pro Phe Gly
515 520 525

Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala Pro Leu Thr Thr
530 535 540

Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile Tyr Ile Gln Gly
545 550 555 560

Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg His Val Lys Arg
565 570 575

Leu His Val Gly Pro Cys Arg *
580

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 91..264

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 265..2487

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 91..2490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCCAGAGC AGACCCGGAT TTCGCTCTTG CGGTCGCTGG GGTTTTAGCA TTGGCTGATC	60
AGTTCGATCC GATCCGGCTG CGAAGGCGAG ATG GCG TTC CGG GTT TCT GGG GCG	114
Met Ala Phe Arg Val Ser Gly Ala	
-58 -55	
GTG CTC GGT GGG GCC GTA AGG GCT CCC CGA CTC ACC GGC GGC GGG GAG	162
Val Leu Gly Gly Ala Val Arg Ala Pro Arg Leu Thr Gly Gly Gly Glu	
-50 -45 -40 -35	
GGT AGT CTA GTC TTC CGG CAC ACC GGC CTC TTC TTA ACT CGG GGT GCT	210
Gly Ser Leu Val Phe Arg His Thr Gly Leu Phe Leu Thr Arg Gly Ala	
-30 -25 -20	
CGA GTT GGA TGT TCG GGG ACG CAC GGG GCC ATG CGC GCG GCG GCC GCG	258
Arg Val Gly Cys Ser Gly Thr His Gly Ala Met Arg Ala Ala Ala Ala	
-15 -10 -5	
GCC AGG AAG GCG GTC ATG GTT CCT GAG GGC GAG AAT GAT GGC CTC GCA	306
Ala Arg Lys Ala Val Met Val Pro Glu Gly Glu Asn Asp Gly Leu Ala	
1 5 10	
TCA AGG GCT GAC TCG GCT CAA TTC CAG TCG GAT GAA CTG GAG GTA CCA	354
Ser Arg Ala Asp Ser Ala Gln Phe Gln Ser Asp Glu Leu Glu Val Pro	
15 20 25 30	

GAC ATT TCT GAA GAG ACA ACG TGC GGT GCT GGT GTG GCT GAT GCT CAA	402
Asp Ile Ser Glu Glu Thr Thr Cys Gly Ala Gly Val Ala Asp Ala Gln	
35 40 45	
GCC TTG AAC AGA GTT CGA GTG GTC CCC CCA CCA AGC GAT GGA CAA AAA	450
Ala Leu Asn Arg Val Arg Val Val Pro Pro Pro Ser Asp Gly Gln Lys	
50 55 60	
ATA TTC CAG ATT GAC CCC ATG TTG CAA GGC TAT AAG TAC CAT CTT GAG	498
Ile Phe Gln Ile Asp Pro Met Leu Gln Gly Tyr Lys Tyr His Leu Glu	
65 70 75	
TAT CGG TAC AGC CTC TAT AGA AGA ATC CGT TCA GAC ATT GAT GAA CAT	546
Tyr Arg Tyr Ser Leu Tyr Arg Arg Ile Arg Ser Asp Ile Asp Glu His	
80 85 90	
GAA GGA GGC TTG GAA GCC TTC TCC CGT AGT TAT GAG AAG TTT GGA TTT	594
Glu Gly Gly Leu Glu Ala Phe Ser Arg Ser Tyr Glu Lys Phe Gly Phe	
95 100 105 110	
AAT GCC AGC GCG GAA GGT ATC ACA TAT CGA GAA TGG GCT CCT GGA GCA	642
Asn Ala Ser Ala Glu Gly Ile Thr Tyr Arg Glu Trp Ala Pro Gly Ala	
115 120 125	
TTT TCT GCA GCA TTG GTG GGT GAC GTC AAC AAC TGG GAT CCA AAT GCA	690
Phe Ser Ala Ala Leu Val Gly Asp Val Asn Asn Trp Asp Pro Asn Ala	
130 135 140	
GAT CGT ATG AGC AAA AAT GAG TTT GGT GTT TGG GAA ATT TTT CTG CCT	738
Asp Arg Met Ser Lys Asn Glu Phe Gly Val Trp Glu Ile Phe Leu Pro	
145 150 155	
AAC AAT GCA GAT GGT ACA TCA CCT ATT CCT CAT GGA TCT CGT GTA AAG	786
Asn Asn Ala Asp Gly Thr Ser Pro Ile Pro His Gly Ser Arg Val Lys	
160 165 170	
GTG AGA ATG GAT ACT CCA TCA GGG ATA AAG GAT TCA ATT CCA GCC TGG	834
Val Arg Met Asp Thr Pro Ser Gly Ile Lys Asp Ser Ile Pro Ala Trp	
175 180 185 190	
ATC AAG TAC TCA GTG CAG GCC CCA GGA GAA ATA CCA TAT GAT GGG ATT	882
Ile Lys Tyr Ser Val Gln Ala Pro Gly Glu Ile Pro Tyr Asp Gly Ile	
195 200 205	
TAT TAT GAT CCT CCT GAA GAG GTA AAG TAT GTG TTC AGG CAT GCG CAA	930

Tyr Tyr Asp Pro Pro Glu Glu Val Lys Tyr Val Phe Arg His Ala Gln	
210 215 220	
CCT AAA CGA CCA AAA TCA TTG CGG ATA TAT GAA ACA CAT GTC GGA ATG	978
Pro Lys Arg Pro Lys Ser Leu Arg Ile Tyr Glu Thr His Val Gly Met	
225 230 235	
AGT AGC CCG GAA CCG AAG ATA AAC ACA TAT GTA AAC TTT AGG GAT GAA	1026
Ser Ser Pro Glu Pro Lys Ile Asn Thr Tyr Val Asn Phe Arg Asp Glu	
240 245 250	
GTC CTC CCA AGA ATA AAA AAA CTT GGA TAC AAT GCA GTG CAA ATA ATG	1074
Val Leu Pro Arg Ile Lys Lys Leu Gly Tyr Asn Ala Val Gln Ile Met	
255 260 265 270	
GCA ATC CAA GAG CAC TCA TAT TAT GGA AGC TTT GGA TAC CAT GTA ACT	1122
Ala Ile Gln Glu His Ser Tyr Tyr Gly Ser Phe Gly Tyr His Val Thr	
275 280 285	
AAT TTT TTT GCG CCA AGT AGT CGT TTT GGT ACC CCA GAA GAT TTG AAG	1170
Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly Thr Pro Glu Asp Leu Lys	
290 295 300	
TCT TTG ATT GAT AGA GCA CAT GAG CTT GGT TTG CTA GTT CTC ATG GAT	1218
Ser Leu Ile Asp Arg Ala His Glu Leu Gly Leu Leu Val Leu Met Asp	
305 310 315	
GTG GTT CAT AGT CAT GCG TCA AGT AAT ACT CTG GAT GGG TTG AAT GGT	1266
Val Val His Ser His Ala Ser Ser Asn Thr Leu Asp Gly Leu Asn Gly	
320 325 330	
TTT GAT GGT ACA GAT ACA CAT TAC TTT CAC AGT GGT CCA CGT GGC CAT	1314
Phe Asp Gly Thr Asp Thr His Tyr Phe His Ser Gly Pro Arg Gly His	
335 340 345 350	
CAC TGG ATG TGG GAT TCT CGC CTA TTT AAC TAT GGG AAC TGG GAA GTT	1362
His Trp Met Trp Asp Ser Arg Leu Phe Asn Tyr Gly Asn Trp Glu Val	
355 360 365	
TTA AGA TTT CTT CTC TCC AAT GCT AGA TGG TGG CTC GAG GAA TAT AAG	1410
Leu Arg Phe Leu Leu Ser Asn Ala Arg Trp Trp Leu Glu Glu Tyr Lys	
370 375 380	
TTT GAT GGT TTC CGT TTT GAT GGT GTG ACC TCC ATG ATG TAC ACT CAC	1458
Phe Asp Gly Phe Arg Phe Asp Gly Val Thr Ser Met Met Tyr Thr His	

385	390	395	
CAC GGA TTA CAA GTA ACA TTT ACG GGG AAC TTC AAT GAG TAT TTT GGC			1506
His Gly Leu Gln Val Thr Phe Thr Gly Asn Phe Asn Glu Tyr Phe Gly			
400	405	410	
TTT GCC ACC GAT GTA GAT GCA GTG GTT TAC TTG ATG CTG GTA AAT GAT			1554
Phe Ala Thr Asp Val Asp Ala Val Val Tyr Leu Met Leu Val Asn Asp			
415	420	425	430
CTA ATT CAT GGA CTT TAT CCT GAG GCT GTA ACC ATT GGT GAA GAT GTT			1602
Leu Ile His Gly Leu Tyr Pro Glu Ala Val Thr Ile Gly Glu Asp Val			
435	440	445	
AGT GGA ATG CCT ACA TTT GCC CTT CCT GTT CAC GAT GGT GGG GTA GGT			1650
Ser Gly Met Pro Thr Phe Ala Leu Pro Val His Asp Gly Gly Val Gly			
450	455	460	
TTT GAC TAT CGG ATG CAT ATG GCT GTG GCT GAC AAA TGG ATT GAC CTT			1698
Phe Asp Tyr Arg Met His Met Ala Val Ala Asp Lys Trp Ile Asp Leu			
465	470	475	
CTC AAG CAA AGT GAT GAA ACT TGG AAG ATG GGT GAT ATT GTG CAC ACA			1746
Leu Lys Gln Ser Asp Glu Thr Trp Lys Met Gly Asp Ile Val His Thr			
480	485	490	
CTG ACA AAT AGG AGG TGG TTA GAG AAG TGT GTA ACT TAT GCT GAA AGT			1794
Leu Thr Asn Arg Arg Trp Leu Glu Lys Cys Val Thr Tyr Ala Glu Ser			
495	500	505	510
CAT GAT CAA GCA TTA GTC GGC GAC AAG ACT ATT GCG TTT TGG TTG ATG			1842
His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu Met			
515	520	525	
GAC AAG GAT ATG TAT GAT TTC ATG GCC CTC GAT AGA CCT TCA ACT CCT			1890
Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Pro			
530	535	540	
ACC ATT GAT CGT GGG ATA GCA TTA CAT AAG ATG ATT AGA CTT ATC ACA			1938
Thr Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Ile Thr			
545	550	555	
ATG GGT TTA GGA GGA GAG GGC TAT CTT AAT TTC ATG GGA AAT GAG TTT			1986
Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe			
560	565	570	

GGA CAT CCT GAA TGG ATA GAT TTT CCA AGA GGT CCG CAA AGA CTT CCA	2034
Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Pro Gln Arg Leu Pro	
575 580 585 590	
AGT GGT AAG TTT ATT CCA GGG AAT AAC AAC AGT TAT GAC AAA TGT CGT	2082
Ser Gly Lys Phe Ile Pro Gly Asn Asn Asn Ser Tyr Asp Lys Cys Arg	
595 600 605	
CGA AGA TTT GAC CTG GGT GAT GCA GAC TAT CTT AGG TAT CAT GGT ATG	2130
Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg Tyr His Gly Met	
610 615 620	
CAA GAG TTT GAT CAG GCA ATG CAA CAT CTT GAG CAA AAA TAT GAA TTC	2178
Gln Glu Phe Asp Gln Ala Met Gln His Leu Glu Gln Lys Tyr Glu Phe	
625 630 635	
ATG ACA TCT GAT CAC CAG TAT ATT TCC CGG AAA CAT GAG GAG GAT AAG	2226
Met Thr Ser Asp His Gln Tyr Ile Ser Arg Lys His Glu Glu Asp Lys	
640 645 650	
GTG ATT GTG TTC GAA AAG GGA GAT TTG GTA TTT GTG TTC AAC TTC CAC	2274
Val Ile Val Phe Glu Lys Gly Asp Leu Val Phe Val Phe Asn Phe His	
655 660 665 670	
TGC AAC AAC AGC TAT TTT GAC TAC CGT ATT GGT TGT CGA AAG CCT GGG	2322
Cys Asn Asn Ser Tyr Phe Asp Tyr Arg Ile Gly Cys Arg Lys Pro Gly	
675 680 685	
GTG TAT AAG GTG GTC TTG GAC TCC GAC GCT GGA CTA TTT GGT GGA TTT	2370
Val Tyr Lys Val Val Leu Asp Ser Asp Ala Gly Leu Phe Gly Gly Phe	
690 695 700	
AGC AGG ATC CAT CAC GCA GCC GAG CAC TTC ACC GCC GAC TGT TCG CAT	2418
Ser Arg Ile His His Ala Ala Glu His Phe Thr Ala Asp Cys Ser His	
705 710 715	
GAT AAT AGG CCA TAT TCA TTC TCG GTT TAT ACA CCA AGC AGA ACA TGT	2466
Asp Asn Arg Pro Tyr Ser Phe Ser Val Tyr Thr Pro Ser Arg Thr Cys	
720 725 730	
GTC GTC TAT GCT CCA GTG GAG TGA TAGCGGGGTA CTCGTTGCTG CGCGGCATGT	2520
Val Val Tyr Ala Pro Val Glu *	
735 740	
GTGGGGCTGT CGATGTGAGG AAAAAACCTTC TTCCAAAACC GGCAGATGCA TGCATGCATG	2580

CTACAATAAG GTTCTGATAC TTTAATCGAT GCTGGAAAGC CCATGCATCT CGCTGCGTTG	2640
TCCTCTCTAT ATATATAAGA CCTTCAAGGT GTCAATTAAA CATAGAGTTT TCGTTTTTCG	2700
CTTTCCTAAA AAAAAAAAAA AAAAA	2725

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Ala	Phe	Arg	Val	Ser	Gly	Ala	Val	Leu	Gly	Gly	Ala	Val	Arg	Ala	-58	-55	-50	-45
Pro	Arg	Leu	Thr	Gly	Gly	Gly	Glu	Gly	Ser	Leu	Val	Phe	Arg	His	Thr	-40	-35	-30	
Gly	Leu	Phe	Leu	Thr	Arg	Gly	Ala	Arg	Val	Gly	Cys	Ser	Gly	Thr	His	-25	-20	-15	
Gly	Ala	Met	Arg	Ala	Ala	Ala	Ala	Ala	Arg	Lys	Ala	Val	Met	Val	Pro	-10	-5	1	5
Glu	Gly	Glu	Asn	Asp	Gly	Leu	Ala	Ser	Arg	Ala	Asp	Ser	Ala	Gln	Phe	10	15	20	
Gln	Ser	Asp	Glu	Leu	Glu	Val	Pro	Asp	Ile	Ser	Glu	Glu	Thr	Thr	Cys	25	30	35	
Gly	Ala	Gly	Val	Ala	Asp	Ala	Gln	Ala	Leu	Asn	Arg	Val	Arg	Val	Val	40	45	50	
Pro	Pro	Pro	Ser	Asp	Gly	Gln	Lys	Ile	Phe	Gln	Ile	Asp	Pro	Met	Leu	55	60	65	70
Gln	Gly	Tyr	Lys	Tyr	His	Leu	Glu	Tyr	Arg	Tyr	Ser	Leu	Tyr	Arg	Arg	75	80	85	

Ile Arg Ser Asp Ile Asp Glu His Glu Gly Gly Leu Glu Ala Phe Ser	90	95	100
Arg Ser Tyr Glu Lys Phe Gly Phe Asn Ala Ser Ala Glu Gly Ile Thr	105	110	115
Tyr Arg Glu Trp Ala Pro Gly Ala Phe Ser Ala Ala Leu Val Gly Asp	120	125	130
Val Asn Asn Trp Asp Pro Asn Ala Asp Arg Met Ser Lys Asn Glu Phe	135	140	145
Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Ala Asp Gly Thr Ser Pro	155	160	165
Ile Pro His Gly Ser Arg Val Lys Val Arg Met Asp Thr Pro Ser Gly	170	175	180
Ile Lys Asp Ser Ile Pro Ala Trp Ile Lys Tyr Ser Val Gln Ala Pro	185	190	195
Gly Glu Ile Pro Tyr Asp Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Val	200	205	210
Lys Tyr Val Phe Arg His Ala Gln Pro Lys Arg Pro Lys Ser Leu Arg	215	220	225
Ile Tyr Glu Thr His Val Gly Met Ser Ser Pro Glu Pro Lys Ile Asn	235	240	245
Thr Tyr Val Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Lys Leu	250	255	260
Gly Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr	265	270	275
Gly Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg	280	285	290
Phe Gly Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His Glu	295	300	305
Leu Gly Leu Leu Val Leu Met Asp Val Val His Ser His Ala Ser Ser	315	320	325

Asn Thr Leu Asp Gly Leu Asn Gly Phe Asp Gly Thr Asp Thr His Tyr	330	335	340
Phe His Ser Gly Pro Arg Gly His His Trp Met Trp Asp Ser Arg Leu	345	350	355
Phe Asn Tyr Gly Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ala	360	365	370
Arg Trp Trp Leu Glu Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly	375	380	385 390
Val Thr Ser Met Met Tyr Thr His His Gly Leu Gln Val Thr Phe Thr	395	400	405
Gly Asn Phe Asn Glu Tyr Phe Gly Phe Ala Thr Asp Val Asp Ala Val	410	415	420
Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly Leu Tyr Pro Glu	425	430	435
Ala Val Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Ala Leu	440	445	450
Pro Val His Asp Gly Gly Val Gly Phe Asp Tyr Arg Met His Met Ala	455	460	465 470
Val Ala Asp Lys Trp Ile Asp Leu Leu Lys Gln Ser Asp Glu Thr Trp	475	480	485
Lys Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu	490	495	500
Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp	505	510	515
Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met	520	525	530
Ala Leu Asp Arg Pro Ser Thr Pro Thr Ile Asp Arg Gly Ile Ala Leu	535	540	545 550
His Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr	555	560	565

Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe	570	575	580
Pro Arg Gly Pro Gln Arg Leu Pro Ser Gly Lys Phe Ile Pro Gly Asn	585	590	595
Asn Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala	600	605	610
Asp Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln	615	620	625
His Leu Glu Gln Lys Tyr Glu Phe Met Thr Ser Asp His Gln Tyr Ile	635	640	645
Ser Arg Lys His Glu Glu Asp Lys Val Ile Val Phe Glu Lys Gly Asp	650	655	660
Leu Val Phe Val Phe Asn Phe His Cys Asn Asn Ser Tyr Phe Asp Tyr	665	670	675
Arg Ile Gly Cys Arg Lys Pro Gly Val Tyr Lys Val Val Leu Asp Ser	680	685	690
Asp Ala Gly Leu Phe Gly Gly Phe Ser Arg Ile His His Ala Ala Glu	695	700	705
His Phe Thr Ala Asp Cys Ser His Asp Asn Arg Pro Tyr Ser Phe Ser	715	720	725
Val Tyr Thr Pro Ser Arg Thr Cys Val Val Tyr Ala Pro Val Glu *	730	735	740

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: transit_peptide

(B) LOCATION: 2..190

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 191..2467

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..2470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

G CTG TGC CTC GTG TCG CCC TCT TCC TCG CCG ACT CCG CTT CCG CCG	46
Leu Cys Leu Val Ser Pro Ser Ser Ser Pro Thr Pro Leu Pro Pro	
-63 -60 -55 -50	
CCG CGG CGC TCT CGC TCG CAT GCT GAT CCG GCG GCA CCG CCG GGG ATC	94
Pro Arg Arg Ser Arg Ser His Ala Asp Arg Ala Ala Pro Pro Gly Ile	
-45 -40 -35	
GCG GGT GGC GGC AAT GTG CGC CTG AGT GTG TTG TCT GTC CAG TGC AAG	142
Ala Gly Gly Gly Asn Val Arg Leu Ser Val Leu Ser Val Gln Cys Lys	
-30 -25 -20	
GCT CGC CGG TCA GGG GTG CGG AAG GTC AAG AGC AAA TTC GCC ACT GCA	190
Ala Arg Arg Ser Gly Val Arg Lys Val Lys Ser Lys Phe Ala Thr Ala	
-15 -10 -5	
GCT ACT GTG CAA GAA GAT AAA ACT ATG GCA ACT GCC AAA GGC GAT GTC	238
Ala Thr Val Gln Glu Asp Lys Thr Met Ala Thr Ala Lys Gly Asp Val	
1 5 10 15	
GAC CAT CTC CCC ATA TAC GAC CTG GAC CCC AAG CTG GAG ATA TTC AAG	286
Asp His Leu Pro Ile Tyr Asp Leu Asp Pro Lys Leu Glu Ile Phe Lys	
20 25 30	
GAC CAT TTC AGG TAC CGG ATG AAA AGA TTC CTA GAG CAG AAA GGA TCA	334
Asp His Phe Arg Tyr Arg Met Lys Arg Phe Leu Glu Gln Lys Gly Ser	
35 40 45	

ATT GAA GAA AAT GAG GGA AGT CTT GAA TCT TTT TCT AAA GGC TAT TTG Ile Glu Glu Asn Glu Gly Ser Leu Glu Ser Phe Ser Lys Gly Tyr Leu 50 55 60	382
AAA TTT GGG ATT AAT ACA AAT GAG GAT GGA ACT GTA TAT CGT GAA TGG Lys Phe Gly Ile Asn Thr Asn Glu Asp Gly Thr Val Tyr Arg Glu Trp 65 70 75 80	430
GCA CCT GCT GCG CAG GAG GCA GAG CTT ATT GGT GAC TTC AAT GAC TGG Ala Pro Ala Ala Gln Glu Ala Glu Leu Ile Gly Asp Phe Asn Asp Trp 85 90 95	478
AAT GGT GCA AAC CAT AAG ATG GAG AAG GAT AAA TTT GGT GTT TGG TCG Asn Gly Ala Asn His Lys Met Glu Lys Asp Lys Phe Gly Val Trp Ser 100 105 110	526
ATC AAA ATT GAC CAT GTC AAA GGG AAA CCT GCC ATC CCT CAC AAT TCC Ile Lys Ile Asp His Val Lys Gly Lys Pro Ala Ile Pro His Asn Ser 115 120 125	574
AAG GTT AAA TTT CGC TTT CTA CAT GGT GGA GTA TGG GTT GAT CGT ATT Lys Val Lys Phe Arg Phe Leu His Gly Gly Val Trp Val Asp Arg Ile 130 135 140	622
CCA GCA TTG ATT CGT TAT GCG ACT GTT GAT GCC TCT AAA TTT GGA GCT Pro Ala Leu Ile Arg Tyr Ala Thr Val Asp Ala Ser Lys Phe Gly Ala 145 150 155 160	670
CCC TAT GAT GGT GTT CAT TGG GAT CCT CCT GCT TCT GAA AGG TAC ACA Pro Tyr Asp Gly Val His Trp Asp Pro Pro Ala Ser Glu Arg Tyr Thr 165 170 175	718
TTT AAG CAT CCT CGG CCT TCA AAG CCT GCT GCT CCA CGT ATC TAT GAA Phe Lys His Pro Arg Pro Ser Lys Pro Ala Ala Pro Arg Ile Tyr Glu 180 185 190	766
GCC CAT GTA GGT ATG AGT GGT GAA AAG CCA GCA GTA AGC ACA TAT AGG Ala His Val Gly Met Ser Gly Glu Lys Pro Ala Val Ser Thr Tyr Arg 195 200 205	814
GAA TTT GCA GAC AAT GTG TTG CCA CGC ATA CGA GCA AAT AAC TAC AAC Glu Phe Ala Asp Asn Val Leu Pro Arg Ile Arg Ala Asn Asn Tyr Asn 210 215 220	862
ACA GTT CAG TTG ATG GCA GTT ATG GAG CAT TCG TAC TAT GCT TCT TTC	910

Thr	Val	Gln	Leu	Met	Ala	Val	Met	Glu	His	Ser	Tyr	Tyr	Ala	Ser	Phe	
225					230					235					240	
GGG	TAC	CAT	GTG	ACA	AAT	TTC	TTT	GCG	GTT	AGC	AGC	AGA	TCA	GGC	ACA	958
Gly	Tyr	His	Val	Thr	Asn	Phe	Phe	Ala	Val	Ser	Ser	Arg	Ser	Gly	Thr	
			245					250						255		
CCA	GAG	GAC	CTC	AAA	TAT	CTT	GTT	GAT	AAG	GCA	CAC	AGT	TTG	GGT	TTG	1006
Pro	Glu	Asp	Leu	Lys	Tyr	Leu	Val	Asp	Lys	Ala	His	Ser	Leu	Gly	Leu	
			260					265					270			
CGA	GTT	CTG	ATG	GAT	GTT	GTC	CAT	AGC	CAT	GCA	AGT	AAT	AAT	GTC	ACA	1054
Arg	Val	Leu	Met	Asp	Val	Val	His	Ser	His	Ala	Ser	Asn	Asn	Val	Thr	
		275					280					285				
GAT	GGT	TTA	AAT	GGC	TAT	GAT	GTT	GGA	CAA	AGC	ACC	CAA	GAG	TCC	TAT	1102
Asp	Gly	Leu	Asn	Gly	Tyr	Asp	Val	Gly	Gln	Ser	Thr	Gln	Glu	Ser	Tyr	
	290					295				300						
TTT	CAT	GCG	GGA	GAT	AGA	GGT	TAT	CAT	AAA	CTT	TGG	GAT	AGT	CGG	CTG	1150
Phe	His	Ala	Gly	Asp	Arg	Gly	Tyr	His	Lys	Leu	Trp	Asp	Ser	Arg	Leu	
305				310				315						320		
TTC	AAC	TAT	GCT	AAC	TGG	GAG	GTA	TTA	AGG	TTT	CTT	CTT	TCT	AAC	CTG	1198
Phe	Asn	Tyr	Ala	Asn	Trp	Glu	Val	Leu	Arg	Phe	Leu	Leu	Ser	Asn	Leu	
			325					330					335			
AGA	TAT	TGG	TTG	GAT	GAA	TTC	ATG	TTT	GAT	GGC	TTC	CGA	TTT	GAT	GGA	1246
Arg	Tyr	Trp	Leu	Asp	Glu	Phe	Met	Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	
		340					345					350				
GTT	ACA	TCA	ATG	CTG	TAT	CAT	CAC	CAT	GGT	ATC	AAT	GTG	GGG	TTT	ACT	1294
Val	Thr	Ser	Met	Leu	Tyr	His	His	His	Gly	Ile	Asn	Val	Gly	Phe	Thr	
	355					360				365						
GGA	AAC	TAC	CAG	GAA	TAT	TTC	AGT	TTG	GAC	ACA	GCT	GTG	GAT	GCA	GTT	1342
Gly	Asn	Tyr	Gln	Glu	Tyr	Phe	Ser	Leu	Asp	Thr	Ala	Val	Asp	Ala	Val	
	370					375				380						
GTT	TAC	ATG	ATG	CTT	GCA	AAC	CAT	TTA	ATG	CAC	AAA	CTC	TTG	CCA	GAA	1390
Val	Tyr	Met	Met	Leu	Ala	Asn	His	Leu	Met	His	Lys	Leu	Leu	Pro	Glu	
385				390				395						400		
GCA	ACT	GTT	GTT	GCT	GAA	GAT	GTT	TCA	GGC	ATG	CCG	GTC	CTT	TGC	CGG	1438
Ala	Thr	Val	Val	Ala	Glu	Asp	Val	Ser	Gly	Met	Pro	Val	Leu	Cys	Arg	

405	410	415	
CCA GTT GAT GAA GGT GGG GTT GGG TTT GAC TAT CGC CTG GCA ATG GCT			1486
Pro Val Asp Glu Gly Gly Val Gly Phe Asp Tyr Arg Leu Ala Met Ala			
420	425	430	
ATC CCT GAT AGA TGG ATT GAC TAC CTG AAG AAT AAA GAT GAC TCT GAG			1534
Ile Pro Asp Arg Trp Ile Asp Tyr Leu Lys Asn Lys Asp Asp Ser Glu			
435	440	445	
TGG TCG ATG GGT GAA ATA GCG CAT ACT TTG ACT AAC AGG AGA TAT ACT			1582
Trp Ser Met Gly Glu Ile Ala His Thr Leu Thr Asn Arg Arg Tyr Thr			
450	455	460	
GAA AAA TGC ATC GCA TAT GCT GAG AGC CAT GAT CAG TCT ATT GTT GGC			1630
Glu Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly			
465	470	475	480
GAC AAA ACT ATT GCA TTT CTC CTG ATG GAC AAG GAA ATG TAC ACT GGC			1678
Asp Lys Thr Ile Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Thr Gly			
485	490	495	
ATG TCA GAC TTG CAG CCT GCT TCA CCT ACA ATT GAT CGA GGG ATT GCA			1726
Met Ser Asp Leu Gln Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala			
500	505	510	
CTC CAA AAG ATG ATT CAC TTC ATC ACA ATG GCC CTT GGA GGT GAT GGC			1774
Leu Gln Lys Met Ile His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly			
515	520	525	
TAC TTG AAT TTT ATG GGA AAT GAG TTT GGT CAC CCA GAA TGG ATT GAC			1822
Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp			
530	535	540	
TTT CCA AGA GAA GGG AAC AAC TGG AGC TAT GAT AAA TGC AGA CGA CAG			1870
Phe Pro Arg Glu Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln			
545	550	555	560
TGG AGC CTT GTG GAC ACT GAT CAC TTG CGG TAC AAG TAC ATG AAT GCG			1918
Trp Ser Leu Val Asp Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala			
565	570	575	
TTT GAC CAA GCG ATG AAT GCG CTC GAT GAG AGA TTT TCC TTC CTT TCG			1966
Phe Asp Gln Ala Met Asn Ala Leu Asp Glu Arg Phe Ser Phe Leu Ser			
580	585	590	

TCG TCA AAG CAG ATC GTC AGC GAC ATG AAC GAT GAG GAA AAG GTT ATT	2014
Ser Ser Lys Gln Ile Val Ser Asp Met Asn Asp Glu Glu Lys Val Ile	
595 600 605	
GTC TTT GAA CGT GGA GAT TTA GTT TTT GTT TTC AAT TTC CAT CCC AAG	2062
Val Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Lys	
610 615 620	
AAA ACT TAC GAG GGC TAC AAA GTG GGA TGC GAT TTG CCT GGG AAA TAC	2110
Lys Thr Tyr Glu Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr	
625 630 635 640	
AGA GTA GCC CTG GAC TCT GAT GCT CTG GTC TTC GGT GGA CAT GGA AGA	2158
Arg Val Ala Leu Asp Ser Asp Ala Leu Val Phe Gly Gly His Gly Arg	
645 650 655	
GTT GGC CAC GAC GTG GAT CAC TTC ACG TCG CCT GAA GGG GTG CCA GGG	2206
Val Gly His Asp Val Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly	
660 665 670	
GTG CCC GAA ACG AAC TTC AAC AAC CGG CCG AAC TCG TTC AAA GTC CTT	2254
Val Pro Glu Thr Asn Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu	
675 680 685	
TCT CCG CCC CGC ACC TGT GTG GCT TAT TAC CGT GTA GAC GAA GCA GGG	2302
Ser Pro Pro Arg Thr Cys Val Ala Tyr Tyr Arg Val Asp Glu Ala Gly	
690 695 700	
GCT GGA CGA CGT CTT CAC GCG AAA GCA GAG ACA GGA AAG ACG TCT CCA	2350
Ala Gly Arg Arg Leu His Ala Lys Ala Glu Thr Gly Lys Thr Ser Pro	
705 710 715 720	
GCA GAG AGC ATC GAC GTC AAA GCT TCC AGA GCT AGT AGC AAA GAA GAC	2398
Ala Glu Ser Ile Asp Val Lys Ala Ser Arg Ala Ser Ser Lys Glu Asp	
725 730 735	
AAG GAG GCA ACG GCT GGT GGC AAG AAG GGA TGG AAG TTT GCG CGG CAG	2446
Lys Glu Ala Thr Ala Gly Gly Lys Lys Gly Trp Lys Phe Ala Arg Gln	
740 745 750	
CCA TCC GAT CAA GAT ACC AAA TGA AGCCACGAGT CCTTGGTGAG GACTGGACTG	2500
Pro Ser Asp Gln Asp Thr Lys *	
755 760	
GCTGCCGGCG CCCTGTTAGT AGTCCTGCTC TACTGGACTA GCCGCCGCTG GCGCCCTTGG	2560

AACGGTCCTT TCCTGTAGCT TGCAGGCGAC TGGTGTCTCA TCACCGAGCA GGCAGGCACT 2620
 GCTTGTATAG CTTTCTAGA ATAATAATCA GGGATGGATG GATGGTGTGT ATTGGCTATC 2680
 TGGCTAGACG TGCATGTGCC CAGTTTGTAT GTACAGGAGC AGTCCCGTC CAGAATAAAA 2740
 AAAAACTTGT TGGGGGGTTT TTC 2763

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Cys Leu Val Ser Pro Ser Ser Ser Pro Thr Pro Leu Pro Pro Pro
 -63 -60 -55 -50

Arg Arg Ser Arg Ser His Ala Asp Arg Ala Ala Pro Pro Gly Ile Ala
 -45 -40 -35

Gly Gly Gly Asn Val Arg Leu Ser Val Leu Ser Val Gln Cys Lys Ala
 -30 -25 -20

Arg Arg Ser Gly Val Arg Lys Val Lys Ser Lys Phe Ala Thr Ala Ala
 -15 -10 -5 1

Thr Val Gln Glu Asp Lys Thr Met Ala Thr Ala Lys Gly Asp Val Asp
 5 10 15

His Leu Pro Ile Tyr Asp Leu Asp Pro Lys Leu Glu Ile Phe Lys Asp
 20 25 30

His Phe Arg Tyr Arg Met Lys Arg Phe Leu Glu Gln Lys Gly Ser Ile
 35 40 45

Glu Glu Asn Glu Gly Ser Leu Glu Ser Phe Ser Lys Gly Tyr Leu Lys
 50 55 60 65

Phe Gly Ile Asn Thr Asn Glu Asp Gly Thr Val Tyr Arg Glu Trp Ala

310	315	320
Asn Tyr Ala Asn Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Leu Arg 325 330 335		
Tyr Trp Leu Asp Glu Phe Met Phe Asp Gly Phe Arg Phe Asp Gly Val 340 345 350		
Thr Ser Met Leu Tyr His His His Gly Ile Asn Val Gly Phe Thr Gly 355 360 365		
Asn Tyr Gln Glu Tyr Phe Ser Leu Asp Thr Ala Val Asp Ala Val Val 370 375 380 385		
Tyr Met Met Leu Ala Asn His Leu Met His Lys Leu Leu Pro Glu Ala 390 395 400		
Thr Val Val Ala Glu Asp Val Ser Gly Met Pro Val Leu Cys Arg Pro 405 410 415		
Val Asp Glu Gly Gly Val Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile 420 425 430		
Pro Asp Arg Trp Ile Asp Tyr Leu Lys Asn Lys Asp Asp Ser Glu Trp 435 440 445		
Ser Met Gly Glu Ile Ala His Thr Leu Thr Asn Arg Arg Tyr Thr Glu 450 455 460 465		
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly Asp 470 475 480		
Lys Thr Ile Ala Phe Leu Leu Met Asp Lys Glu Met Tyr Thr Gly Met 485 490 495		
Ser Asp Leu Gln Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu 500 505 510		
Gln Lys Met Ile His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr 515 520 525		
Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe 530 535 540 545		
Pro Arg Glu Gly Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp		

550	555	560
Ser Leu Val Asp Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe		
565	570	575
Asp Gln Ala Met Asn Ala Leu Asp Glu Arg Phe Ser Phe Leu Ser Ser		
580	585	590
Ser Lys Gln Ile Val Ser Asp Met Asn Asp Glu Glu Lys Val Ile Val		
595	600	605
Phe Glu Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Lys Lys		
610	615	620 625
Thr Tyr Glu Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg		
630	635	640
Val Ala Leu Asp Ser Asp Ala Leu Val Phe Gly Gly His Gly Arg Val		
645	650	655
Gly His Asp Val Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly Val		
660	665	670
Pro Glu Thr Asn Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu Ser		
675	680	685
Pro Pro Arg Thr Cys Val Ala Tyr Tyr Arg Val Asp Glu Ala Gly Ala		
690	695	700 705
Gly Arg Arg Leu His Ala Lys Ala Glu Thr Gly Lys Thr Ser Pro Ala		
710	715	720
Glu Ser Ile Asp Val Lys Ala Ser Arg Ala Ser Ser Lys Glu Asp Lys		
725	730	735
Glu Ala Thr Ala Gly Gly Lys Lys Gly Trp Lys Phe Ala Arg Gln Pro		
740	745	750
Ser Asp Gln Asp Thr Lys *		
755	760	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG GCG ACG CCC TCG GCC GTG GGC GCC GCG TGC CTC CTC CTC GCG CGG	48
Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg	
765 770 775	
GCC GCC TGG CCG GCC GCC GTC GGC GAC CGG GCG CGC CCG CGG AGG CTC	96
Ala Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu	
780 785 790	
CAG CGC GTG CTG CGC CGC CGG TGC GTC GCG GAG CTG AGC AGG GAG GGG	144
Gln Arg Val Leu Arg Arg Arg Cys Val Ala Glu Leu Ser Arg Glu Gly	
795 800 805	
CCC CAT ATG	153
Pro His Met	
810	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg
 1 5 10 15

Ala Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu
 20 25 30

Gln Arg Val Leu Arg Arg Arg Cys Val Ala Glu Leu Ser Arg Glu Gly
 35 40 45

Pro His Met
 50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGC GTC GCG GAG CTG AGC AGG GAG GAC CTC GGT CTC GAA CCT GAA GGG	48
Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly	
55 60 65	
ATT GCT GAA GGT TCC ATC GAT AAC ACA GTA GTT GTG GCA AGT GAG CAA	96
Ile Ala Glu Gly Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln	
70 75 80	
GAT TCT GAG ATT GTG GTT GGA AAG GAG CAA GCT CGA GCT AAA GTA ACA	144
Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr	
85 90 95	
CAA AGC ATT GTC TTT GTA ACC GGC GAA GCT TCT CCT TAT GCA AAG TCT	192

Gln	Ser	Ile	Val	Phe	Val	Thr	Gly	Glu	Ala	Ser	Pro	Tyr	Ala	Lys	Ser	
100					105					110					115	
GGG	GGT	CTA	GGA	GAT	GTT	TGT	GGT	TCA	TTG	CCA	GTT	GCT	CTT	GCT	GCT	240
Gly	Gly	Leu	Gly	Asp	Val	Cys	Gly	Ser	Leu	Pro	Val	Ala	Leu	Ala	Ala	
				120					125					130		
CGT	GGT	CAC	CGT	GTG	ATG	GTT	GTA	ATG	CCC	AGA	TAT	TTA	AAT	GGT	ACC	288
Arg	Gly	His	Arg	Val	Met	Val	Val	Met	Pro	Arg	Tyr	Leu	Asn	Gly	Thr	
			135					140					145			
TCC	GAT	AAG	AAT	TAT	GCA	AAT	GCA	TTT	TAC	ACA	CAA	AAA	CAC	ATT	CGG	336
Ser	Asp	Lys	Asn	Tyr	Ala	Asn	Ala	Phe	Tyr	Thr	Glu	Lys	His	Ile	Arg	
		150					155					160				
ATT	CCA	TGC	TTT	GGC	GGT	GAA	CAT	GAA	GTT	ACC	TTC	TTC	CAT	GAG	TAT	384
Ile	Pro	Cys	Phe	Gly	Gly	Glu	His	Glu	Val	Thr	Phe	Phe	His	Glu	Tyr	
	165					170				175						
AGA	GAT	TCA	GTT	GAC	TGG	GTG	TTT	GTT	GAT	CAT	CCC	TCA	TAT	CAC	AGA	432
Arg	Asp	Ser	Val	Asp	Trp	Val	Phe	Val	Asp	His	Pro	Ser	Tyr	His	Arg	
180				185					190						195	
CCT	GGA	AAT	TTA	TAT	GGA	GAT	AAG	TTT	GGT	GCT	TTT	GGT	GAT	AAT	CAG	480
Pro	Gly	Asn	Leu	Tyr	Gly	Asp	Lys	Phe	Gly	Ala	Phe	Gly	Asp	Asn	Gln	
			200					205					210			
TTC	AGA	TAC	ACA	CTC	CTT	TGC	TAT	GCT	GCA	TGT	GAG	GCT	CCT	TTG	ATC	528
Phe	Arg	Tyr	Thr	Leu	Leu	Cys	Tyr	Ala	Ala	Cys	Glu	Ala	Pro	Leu	Ile	
			215				220					225				
CTT	GAA	TTG	GGA	GGA	TAT	ATT	TAT	GGA	CAG	AAT	TGC	ATG	TTT	GTT	GTC	576
Leu	Glu	Leu	Gly	Gly	Tyr	Ile	Tyr	Gly	Gln	Asn	Cys	Met	Phe	Val	Val	
	230					235					240					
AAT	GAT	TGG	CAT	GCC	AGT	CTA	GTG	CCA	GTC	CTT	CTT	GCT	GCA	AAA	TAT	624
Asn	Asp	Trp	His	Ala	Ser	Leu	Val	Pro	Val	Leu	Leu	Ala	Ala	Lys	Tyr	
	245					250				255						
AGA	CCA	TAT	GGT	GTT	TAT	AAA	GAC	TCC	CGC	AGC	ATT	CTT	GTA	ATA	CAT	672
Arg	Pro	Tyr	Gly	Val	Tyr	Lys	Asp	Ser	Arg	Ser	Ile	Leu	Val	Ile	His	
260				265					270					275		
AAT	TTA	GCA	CAT	CAG	GGT	GTA	GAG	CCT	GCA	AGC	ACA	TAT	CCT	GAC	CTT	720
Asn	Leu	Ala	His	Gln	Gly	Val	Glu	Pro	Ala	Ser	Thr	Tyr	Pro	Asp	Leu	

280	285	290	
GGG TTG CCA CCT GAA TGG TAT GGA GCT CTG GAG TGG GTA TTC CCT GAA			768
Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu			
295	300	305	
TGG GCG AGG AGG CAT GCC CTT GAC AAG GGT GAG GCA GTT AAT TTT TTG			816
Trp Ala Arg Arg His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu			
310	315	320	
AAA GGT GCA GTT GTG ACA GCA GAT CGA ATC GTG ACT GTC AGT AAG GGT			864
Lys Gly Ala Val Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly			
325	330	335	
TAT TCG TGG GAG GTC ACA ACT GCT GAA GGT GGA CAG GGC CTC AAT GAG			912
Tyr Ser Trp Glu Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu			
340	345	350	355
CTC TTA AGC TCC AGA AAG AGT GTA TTA AAC GGA ATT GTA AAT GGA ATT			960
Leu Leu Ser Ser Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile			
360	365	370	
GAC ATT AAT GAT TGG AAC CCT GCC ACA GAC AAA TGT ATC CCC TGT CAT			1008
Asp Ile Asn Asp Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His			
375	380	385	
TAT TCT GTT GAT GAC CTC TCT GGA AAG GCC AAA TGT AAA GGT GCA TTG			1056
Tyr Ser Val Asp Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu			
390	395	400	
CAG AAG GAG CTG GGT TTA CCT ATA AGG CCT GAT GTT CCT CTG ATT GGC			1104
Gln Lys Glu Leu Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly			
405	410	415	
TTT ATT GGA AGG TTG GAT TAT CAG AAA GGC ATT GAT CTC ATT CAA CTT			1152
Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu			
420	425	430	435
ATC ATA CCA GAT CTC ATG CGG GAA GAT GTT CAA TTT GTC ATG CTT GGA			1200
Ile Ile Pro Asp Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly			
440	445	450	
TCT GGT GAC CCA GAG CTT GAA GAT TGG ATG AGA TCT ACA GAG TCG ATC			1248
Ser Gly Asp Pro Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile			
455	460	465	

TTC AAG GAT AAA TTT CGT GGA TGG GTT GGA TTT AGT GTT CCA GTT TCC	1296
Phe Lys Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser	
470 475 480	
CAC CGA ATA ACT GCC GGC TGC GAT ATA TTG TTA ATG CCA TCC AGA TTC	1344
His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe	
485 490 495	
GAA CCT TGT GGT CTC AAT CAG CTA TAT GCT ATG CAG TAT GGC ACA GTT	1392
Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val	
500 505 510 515	
CCT GTT GTC CAT GCA ACT GGG GGC CTT AGA GAT ACC GTG GAG AAC TTC	1440
Pro Val Val His Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe	
520 525 530	
AAC CCT TTC GGT GAG AAT GGA GAG CAG GGT ACA GGG TGG GCA TTC GCA	1488
Asn Pro Phe Gly Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala	
535 540 545	
CCC CTA ACC ACA GAA AAC ATG TTT GTG GAC ATT GCG AAC TGC AAT ATC	1536
Pro Leu Thr Thr Glu Asn Met Phe Val Asp Ile Ala Asn Cys Asn Ile	
550 555 560	
TAC ATA CAG GGA ACA CAA GTC CTC CTG GGA AGG GCT AAT GAA GCG AGG	1584
Tyr Ile Gln Gly Thr Gln Val Leu Leu Gly Arg Ala Asn Glu Ala Arg	
565 570 575	
CAT GTC AAA AGA CTT CAC GTG GGA CCA TGC CGC TGA	1620
His Val Lys Arg Leu His Val Gly Pro Cys Arg *	
580 585 590	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Val Ala Glu Leu Ser Arg Glu Asp Leu Gly Leu Glu Pro Glu Gly

1	5	10	15
Ile Ala Glu Gly Ser Ile Asp Asn Thr Val Val Val Ala Ser Glu Gln			
20	25	30	
Asp Ser Glu Ile Val Val Gly Lys Glu Gln Ala Arg Ala Lys Val Thr			
35	40	45	
Gln Ser Ile Val Phe Val Thr Gly Glu Ala Ser Pro Tyr Ala Lys Ser			
50	55	60	
Gly Gly Leu Gly Asp Val Cys Gly Ser Leu Pro Val Ala Leu Ala Ala			
65	70	75	80
Arg Gly His Arg Val Met Val Val Met Pro Arg Tyr Leu Asn Gly Thr			
85	90	95	
Ser Asp Lys Asn Tyr Ala Asn Ala Phe Tyr Thr Glu Lys His Ile Arg			
100	105	110	
Ile Pro Cys Phe Gly Gly Glu His Glu Val Thr Phe Phe His Glu Tyr			
115	120	125	
Arg Asp Ser Val Asp Trp Val Phe Val Asp His Pro Ser Tyr His Arg			
130	135	140	
Pro Gly Asn Leu Tyr Gly Asp Lys Phe Gly Ala Phe Gly Asp Asn Gln			
145	150	155	160
Phe Arg Tyr Thr Leu Leu Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile			
165	170	175	
Leu Glu Leu Gly Gly Tyr Ile Tyr Gly Gln Asn Cys Met Phe Val Val			
180	185	190	
Asn Asp Trp His Ala Ser Leu Val Pro Val Leu Leu Ala Ala Lys Tyr			
195	200	205	
Arg Pro Tyr Gly Val Tyr Lys Asp Ser Arg Ser Ile Leu Val Ile His			
210	215	220	
Asn Leu Ala His Gln Gly Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu			
225	230	235	240
Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu			

245	250	255
Trp Ala Arg Arg His Ala Leu Asp Lys Gly Glu Ala Val Asn Phe Leu		
260	265	270
Lys Gly Ala Val Val Thr Ala Asp Arg Ile Val Thr Val Ser Lys Gly		
275	280	285
Tyr Ser Trp Glu Val Thr Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu		
290	295	300
Leu Leu Ser Ser Arg Lys Ser Val Leu Asn Gly Ile Val Asn Gly Ile		
305	310	315 320
Asp Ile Asn Asp Trp Asn Pro Ala Thr Asp Lys Cys Ile Pro Cys His		
325	330	335
Tyr Ser Val Asp Asp Leu Ser Gly Lys Ala Lys Cys Lys Gly Ala Leu		
340	345	350
Gln Lys Glu Leu Gly Leu Pro Ile Arg Pro Asp Val Pro Leu Ile Gly		
355	360	365
Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile Asp Leu Ile Gln Leu		
370	375	380
Ile Ile Pro Asp Leu Met Arg Glu Asp Val Gln Phe Val Met Leu Gly		
385	390	395 400
Ser Gly Asp Pro Glu Leu Glu Asp Trp Met Arg Ser Thr Glu Ser Ile		
405	410	415
Phe Lys Asp Lys Phe Arg Gly Trp Val Gly Phe Ser Val Pro Val Ser		
420	425	430
His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu Met Pro Ser Arg Phe		
435	440	445
Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met Gln Tyr Gly Thr Val		
450	455	460
Pro Val Val His Ala Thr Gly Gly Leu Arg Asp Thr Val Glu Asn Phe		
465	470	475 480
Asn Pro Phe Gly Glu Asn Gly Glu Gln Gly Thr Gly Trp Ala Phe Ala		

	485		490		495										
Pro	Leu	Thr	Thr	Glu	Asn	Met	Phe	Val	Asp	Ile	Ala	Asn	Cys	Asn	Ile
				500					505					510	
Tyr	Ile	Gln	Gly	Thr	Gln	Val	Leu	Leu	Gly	Arg	Ala	Asn	Glu	Ala	Arg
		515					520						525		
His	Val	Lys	Arg	Leu	His	Val	Gly	Pro	Cys	Arg	*				
		530				535					540				

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGGATCCAT GGCGACGCCC TCGGCCGTGG

30

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGAATTCCA TATGGGGCCC CTCCCTGCTC AGCTC

35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCTGAGCTC AAGCTTGCTA CTTTCTTTCC TTAATG

36

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTCTCCGCGG TGGTGTCTT GCTTCCTAG

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCGTCGCGG AGCTGAGCAG GGAGGTCTCC GCGGTGGTGT CCTTGCTTCC TAG

53

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Val Ala Glu Leu Ser Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGAGAGAGAG AGAGAG

16

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGAAGAAGA AGAAGAAGAA GAAGAAGAAG AAGAAG

36

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAAAAAAAA AAAAAAAAAA

18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATAATGCA G

11

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AACAATGGCT

10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO..

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ala Ser Ser Met Leu Ser Ser Ala Ala Val Ala Thr Arg Thr Asn
1 5 10 15

Pro Ala Gln Ala Ser Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ala
 20 25 30

Ala Phe Pro Val Ser Arg Lys Gln Asn Leu Asp Ile Thr Ser Ile Ala
 35 40 45

Ser Asn Gly Gly Arg Val Gln Cys
 50 55

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Pro Thr Val Met Met Ala Ser Ser Ala Thr Ala Thr Arg Thr
1 5 10 15

Asn Pro Ala Gln Ala Ser Ala Val Ala Pro Phe Gln Gly Leu Lys Ser
 20 25 30

Thr Ala Ser Leu Pro Val Ala Arg Arg Ser Ser Arg Ser Leu Gly Asn

Val Ala Ser Asn Gly Gly Arg Ile Arg Cys
50 55

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Ala Gln Ile Leu Ala Pro Ser Thr Gln Trp Gln Met Arg Ile Thr
1 5 10 15

Lys Thr Ser Pro Cys Ala Thr Pro Ile Thr Ser Lys Met Trp Ser Ser
20 25 30

Leu Val Met Lys Gln Thr Lys Lys Val Ala His Ser Ala Lys Phe Arg
35 40 45

Val Met Ala Val Asn Ser Glu Asn Gly Thr
50 55

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly His
1 5 10 15
Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly Leu
 20 25 30
Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg Thr
 35 40 45
Ser Ala Arg Ala Ala Pro Arg His Gln Gln Gln Ala Arg Arg Gly Gly
 50 55 60
Arg Phe Pro Phe Pro Ser Leu Val Val Cys
65 70

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ala Thr Pro Ser Ala Val Gly Ala Ala Cys Leu Leu Leu Ala Arg
1 5 10 15
Xaa Ala Trp Pro Ala Ala Val Gly Asp Arg Ala Arg Pro Arg Arg Leu
 20 25 30
Gln Arg Val Leu Arg Arg Arg
 35